

GenCore version 5.1.4 p5 4578
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 OM protein - protein search, using SW model
 Run on: April 12, 2003, 08:39:44 ; Search time 16 Seconds
 (without alignments)
 951.430 Million cell updates/sec

Title: US-09-905-810-2
 Perfect score: 1268
 Sequence: 1 MAARSQRERRGRGPGTAL.....PWAHLKAAPFLTYGLFQVH 249

Scoring table: BLOSUM62
 Gapext 0.5

searched: 248812 seqs, 61136040 residues

all number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database :

Published Applications AA:*

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- /cgn2_6_ptodata/2/pubpaa/us60 PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1268	100.0	249	10 US-09-905-810-2	Sequence 2, Appli
2	1268	100.0	249	10 US-09-78-980-44	Sequence 44, Appli
3	1066	84.1	273	10 US-09-74-454A-2	Sequence 2, Appli
4	1066	84.1	273	10 US-09-883-777-2	Sequence 2, Appli
5	1020	80.4	225	10 US-09-905-10-1	Sequence 1, Appli
6	116	9.1	409	10 US-09-813-329-6	Sequence 6, Appli
7	105.5	8.3	405	10 US-09-813-329-4	Sequence 4, Appli
8	104	8.2	409	10 US-09-813-329-2	Sequence 2, Appli
9	92.5	7.3	208	10 US-09-027-287-39	Sequence 39, Appli
10	92.5	7.3	208	10 US-09-257-656B-39	Sequence 39, Appli
11	91.5	7.2	240	9 US-09-967-604-6	Sequence 6, Appli
12	91.5	7.2	240	9 US-10-151-882-45	Sequence 45, Appli
13	91.5	7.2	240	10 US-09-027-287-45	Sequence 2, Appli
14	91.5	7.2	240	10 US-09-252-656B-2	Sequence 2, Appli
15	91.5	7.1	240	12 US-10-066-209-4	Sequence 4, Appli
16	90	7.1	660	12 US-10-115-178-1	Sequence 1, Appli
17	88	6.9	373	9 US-10-174-590-372	Sequence 37, App
18	88	6.9	373	9 US-10-176-758-372	Sequence 372, App
19	88	6.9	373	9 US-10-175-737-372	Sequence 372, App

ALIGNMENTS

RESULT 1
 US-09-905-810-2
 ; Sequence 2, Application US/0905810
 ; Patent No. US2000015705AI
 ; GENERAL INFORMATION
 ; APPLICANT: BIOPEN, INC.
 ; ATTORNEY: RENNERT, Paul
 ; TITLE OF INVENTION: Antagonists of Tweak and of Tweak Receptors and Their Use to Treat Immunological Disorders
 ; FILE REFERENCE: A06 US
 ; CURRENT FILING DATE: 2001-07-13
 ; PRIOR APPLICATION NUMBER: PCT/US00/01044
 ; PRIOR FILING DATE: 2000-01-14
 ; PRIOR APPLICATION NUMBER: 60/116,168
 ; PRIOR FILING DATE: 1999-01-15
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 249
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-09-905-810-2

Db 181 LLVDGVLAIRCLEEFSATAASSLGQLQLCQVSGLLAURPQSSLRIRTLPAWHLKAAPFL 240
 Qy 241 TYFGLFQVH 249
 Db 241 TYFGLFQVH 249

RESULT 2
 US-09-782-980-44
 Sequence 44, Application US/09782980
 Patent No. US20020072089A1
 GENERAL INFORMATION:
 APPLICANT: Khodadoust, Mehran M.
 APPLICANT: Macbeth, Kylie J.
 APPLICANT: Busfield, Samantha J.
 APPLICANT: McCarthy, Sean A.
 APPLICANT: Holtzman, Douglas A.
 APPLICANT: Gu, Wei
 APPLICANT: White, David
 APPLICANT: Pan, Yang

TITLE OF INVENTION: NOVEL, ITALY, LOR-2, STRIVE, TRASH, BDSF, LRSF, AND
 TITLE OF INVENTION: STMST PROTEIN AND NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION: THEREFOP
 FILE REFERENCE: MNI-121CP
 CURRENT APPLICATION NUMBER: US/09/782,980
 CURRENT FILING DATE: 2001-02-13
 PRIOR APPLICATION: PCT/US00/02125
 PRIOR FILING DATE: 2000-01-27
 PRIOR APPLICATION NUMBER: 09/448,076
 PRIOR FILING DATE: 1999-11-23
 PRIOR APPLICATION NUMBER: 09/276,400
 PRIOR FILING DATE: 1999-03-25
 PRIOR APPLICATION: PCT/US00/02125
 PRIOR FILING DATE: 2000-01-27
 PRIOR APPLICATION NUMBER: 09/448,076
 PRIOR FILING DATE: 1999-11-23
 PRIOR APPLICATION NUMBER: 09/276,400
 PRIOR FILING DATE: 1999-03-25
 PRIOR FILING DATE: 1999-01-27
 PRIOR FILING DATE: 1998-01-27
 PRIOR APPLICATION NUMBER: 09/014,195
 PRIOR FILING DATE: 1998-01-27
 PRIOR APPLICATION NUMBER: 09/014,348
 PRIOR FILING DATE: 1998-01-27
 NUMBER OF SEQ ID NOS: 176
 SOFTWARE: PatentIn Ver. 2.0
 LENGTH: 249
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-782-980-44

Qy 121 GAQAGVDTGTVSSWEARINSSPLRVNQIGEFIVTRAGLYLYCQHDEGGKAVYLKLD 180
 Db 121 GQQAGVDTGTVSSWEARINSSPLRVNQIGEFIVTRAGLYLYCQHDEGGKAVYLKLD 180
 Qy 181 LLVDGVLAIRCLEEFSATAASSLGQLQLCQVSGLLAURPQSSLRIRTLPAWHLKAAPFL 240
 Db 181 LLVDGVLAIRCLEEFSATAASSLGQLQLCQVSGLLAURPQSSLRIRTLPAWHLKAAPFL 240

RESULT 3
 US-09-742-454A-2
 Sequence 2, Application US/09742454A
 Patent No. US2002001876A1
 GENERAL INFORMATION:
 APPLICANT: WILEY, Steven R.
 TITLE OF INVENTION: TWEAK Receptor
 FILE REFERENCE: 2968-B
 CURRENT APPLICATION NUMBER: US/09/742,454A
 CURRENT FILING DATE: 2000-12-19
 PRIOR APPLICATION NUMBER: 60/172,878
 PRIOR FILING DATE: 1999-12-20
 PRIOR APPLICATION NUMBER: 60/203,347
 PRIOR FILING DATE: 2000-05-10
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 2
 LENGTH: 273
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: human TWEAK
 OTHER INFORMATION: Description of Artificial Sequence: human TWEAK
 OTHER INFORMATION: fusion protein construct
 US-09-742-454A-2

Query Match 84.1%; Score 1066; DB 10;
 Best Local Similarity 100.0%; Pred. No. 1.8e-89;
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 Db 67 SIGSRASLSAQPAQELVAAEDQDPSELNQTEESQDPAPFLNVRPRSAPKGRKTR 126

Qy 103 ARRAIAAHYEVPRPGDGAQGVDTVSGMEARINSSPRLYRNQIGEFIVTRAGLYY 162
 Db 127 ARRAIAAHYEVPRPGDGAQGVDTVSGMEARINSSPRLYRNQIGEFIVTRAGLYY 186

Qy 163 LYCQVHDEGGKAVYLKLDLLYDGVLAIRCLBEFSATAASSLGQLQLCQVSGLLAURPGS 222
 Db 187 LYCQVHDEGGKAVYLKLDLLYDGVLAIRCLBEFSATAASSLGQLQLCQVSGLLAURPGS 246

Qy 223 SIRIRTLPAWHLKAAPFLTYFGLFQVH 249
 Db 247 SIRIRTLPAWHLKAAPFLTYFGLFQVH 273

RESULT 4
 US-09-883-777-2
 Sequence 2, Application US/09883777
 Patent No. US2002011085A1
 GENERAL INFORMATION:
 APPLICANT: WILEY, Steven R.
 TITLE OF INVENTION: TWEAK RECEPTOR
 FILE REFERENCE: 2968-C
 CURRENT FILING DATE: 2001-06-18
 PRIOR APPLICATION NUMBER: US 60/172,878
 PRIOR FILING DATE: 1999-12-20
 PRIOR APPLICATION NUMBER: US 60/203,347
 PRIOR APPLICATION NUMBER: US 60/203,347

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 12, 2003, 08:38:12 ; Search time 36 Seconds

(without alignments)
 921.650 Million cell updates/sec

Perfect score: US-09-905-810-2

Sequence: 1 MAARRSQRERRGRGEPTAL.....PWAHLKAPFLTYFGLFQVH 249

Scoring table: BLOSUM62

Gapext 0.5

Searched: 908470 seqs, 133250620 residues

.1 number of hits satisfying chosen parameters: 908470

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1268	100.0	249	20	AAV09369	Human tumour necro
2	1268	100.0	249	21	AAV07526	Amino acid sequenc
3	1268	100.0	249	23	AAV95338	Human PRO207 antit
4	1268	100.0	249	23	AAU86129	Human PRO207 polyP
5	1268	100.0	284	19	AAW47525	Homo sapiens tumou
6	1265	99.8	249	19	AAW29745	TNF related endoth
7	1265	99.8	249	22	AAE00891	Human TREPA (TNF r
8	1066	84.1	273	22	AAU03499	TWEAK extracellular
9	1062	83.8	208	20	AAW9350	Human TNRL3 protei
10	1020	80.4	225	19	AAW47524	Mus musculus tumou

OS Homo sapiens.
 XX WO9319490-A1.

XX

Result No.	Score	Query	Match	Length	DB ID	Description
1	1268	100.0	249	20	AAV09369	Human tumour necro
2	1268	100.0	249	21	AAV07526	Amino acid sequenc
3	1268	100.0	249	23	AAV95338	Human PRO207 antit
4	1268	100.0	249	23	AAU86129	Human PRO207 polyP
5	1268	100.0	284	19	AAW47525	Homo sapiens tumou
6	1265	99.8	249	19	AAW29745	TNF related endoth
7	1265	99.8	249	22	AAE00891	Human TREPA (TNF r
8	1066	84.1	273	22	AAU03499	TWEAK extracellular
9	1062	83.8	208	20	AAW9350	Human TNRL3 protei
10	1020	80.4	225	19	AAW47524	Mus musculus tumou

PT New human Apo-3 ligand (a tumour necrosis factor) homologue

ALIGNMENTS

RESULT 1
 ID AAY09369 standard; Protein; 249 AA.

XX

xx Claim 1; Fig 1; 74pp; English.
 xx The present sequence represents a human tumour necrosis factor (TNF) and lymphotoxin homologue designated Apo-3 ligand. Apo-3 ligand has cytostatic activity. Apo-3 ligand can be used to induce apoptosis in mammalian cancer cells, to induce NF- κ B-dependent transcription and to induce JNK/SAPK-dependent responses in mammalian cells.
 xx Sequence 249 AA;

Query Match 100.0%; Score 1268; DB 20; Length 249;
 Best Local Similarity 100.0%; Fred. No. 1.4e-119; Gaps 0;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Query 1 MAARRSQRGRGRGEPTGTTLVLPLAIGLGLACLGLLAVSLSGRASLSAQEPQEL 60
 Db 1 MAARRSQRGRGRGEPTGTTLVLPLAIGLGLACLGLLAVSLSGRASLSAQEPQEL 60
 Qv 61 VAAEQQDPSELNPQTEESDQAPAPFLVLRPRTSAPKGRKTRARRAAAHYEVHPRGQD 120
 61 VAAEQQDPSELNPQTEESDQAPAPFLVLRPRTSAPKGRKTRARRAAAHYEVHPRGQD 120
 Qy 121 GAOAGVDTGTVSGWEARINSSPFLRQIGEFITRAGLYLYCQVHDEGKAVYLKD 180
 Db 121 GAOAGVDTGTVSGWEARINSSPFLRQIGEFITRAGLYLYCQVHDEGKAVYLKD 180
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 Db 181 LLVDGVLAIRCLLEFFSATAASSLGPQLRCOVSGLLALRPGSSLRIRTLPWAHKAAPFL 240
 Qy 241 TYFGLFQVH 249
 Db 241 TYFGLFQVH 249

RESULT 2
 AAB07526
 ID AAB07526 standard; protein; 249 AA.
 AC AAB07526;
 XX DT 20-OCT-2000 (first entry)

DE Amino acid sequence of a soluble recombinant human TWEAK protein.
 XX TWEAK protein; immunological disorder; immune response; inflammation; TWEAK blocking agent; autoimmune disease; organ transplant rejection; Graft-versus-Host disease; GVHD; lymphoid cell malignancy; shock; tumour; Homo sapiens.
 XX WO200042073-A1.
 XX PD 20-JUL-2000.

XX PF 14-JAN-2000; 2000WO-US01044.

XX PR 15-JAN-1999; 99US-0116168.
 XX PA (BIOJ) BIOGEN INC.

XX PI Bennett P;

XX DR WPI: 2000-476036/41.

XX Preventing and treating immune responses using modulators, especially antibodies of TWEAK receptors and TWEAK ligands, useful for treating e.g. inflammation and Graft versus host disease - Disclosure; Fig 1; 45pp; English.
 XX The present sequence represents a TWEAK protein. The specification

describes a method for preventing or treating an immunological disorder and/or inhibiting an immune response in an animal. The method comprises administering a TWEAK blocking agent. The method may be used for preventing and treating immune disorders associated with inappropriate expression and/or activity of TWEAK. These disorders include autoimmune diseases, acute and chronic inflammation, organ transplant rejection; Graft-versus-Host disease (GVHD), lymphoid cell malignancies, septic and other forms of shock, loss of immune responsiveness (as seen in human immunodeficiency virus (HIV) infections) and failure of the immune response to tumour growth.
 xx Sequence 249 AA;

Query Match 100.0%; Score 1268; DB 21; Length 249;
 Best Local Similarity 100.0%; Fred. No. 1.4e-119; Gaps 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 1 MAARRSQRGRGRGEPTGTTLVLPLAIGLGLACLGLLAVSLSGRASLSAQEPQEL 60
 Qy 61 VAAEQQDPSELNPQTEESDQAPAPFLVLRPRTSAPKGRKTRARRAAAHYEVHPRGQD 120
 Db 61 VAAEQQDPSELNPQTEESDQAPAPFLVLRPRTSAPKGRKTRARRAAAHYEVHPRGQD 120
 Qy 61 VAAEQQDPSELNPQTEESDQAPAPFLVLRPRTSAPKGRKTRARRAAAHYEVHPRGQD 120
 Db 61 VAAEQQDPSELNPQTEESDQAPAPFLVLRPRTSAPKGRKTRARRAAAHYEVHPRGQD 120
 Qy 121 GAOAGVDTGTVSGWEARINSSPFLRQIGEFITRAGLYLYCQVHDEGKAVYLKD 180
 Db 121 GAOAGVDTGTVSGWEARINSSPFLRQIGEFITRAGLYLYCQVHDEGKAVYLKD 180
 Qy 181 LLVDGVLAIRCLLEFFSATAASSLGPQLRCOVSGLLALRPGSSLRIRTLPWAHKAAPFL 240
 Db 181 LLVDGVLAIRCLLEFFSATAASSLGPQLRCOVSGLLALRPGSSLRIRTLPWAHKAAPFL 240
 Qy 241 TYFGLFQVH 249
 Db 241 TYFGLFQVH 249

RESULT 3
 AAY95338
 ID AAY95338 standard; Protein; 249 AA.
 XX AC AAY95338;
 XX DT 25-SEP-2000 (first entry)
 XX DE Human PRO207 antitumour protein.
 XX KW PRO207; human; antitumour; tumour; therapy; cytostatic; breast cancer; ovarian cancer; renal cancer; colorectal cancer; uterine cancer; prostate cancer; lung cancer; bladder cancer; central nervous system cancer; melanoma; leukaemia; neoplasm.
 XX OS Homo sapiens.
 XX FH Key Peptide 1-40
 FT Label= Signal_peptide
 FT Protein 41-249
 FT Label= PRO207
 FT Modified-site 27..33
 FT Modified-site 29..35
 FT Modified-site /note= "N-myristoylation"
 FT Modified-site 36..42
 FT Modified-site /note= "N-myristoylation"
 FT Modified-site 45..51
 FT Modified-site 118..124
 FT Modified-site /note= "N-myristoylation"
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 FT Modified-site /note= "N-myristoylation"
 FT Modified-site 125..131

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FT	Modified-site	128 . 134	Qy	181 LLVDEVLAIRCLEEFSATAASSLGFLQRLCQVSGILLARPGSLIRITLDEWAHJKAAPFL 240
FT	Modified-site	139 . 143	Db	181 LLVDEVLAIRCLEEFSATAASSLGFLQRLCQVSGILLARPGSLIRITLDEWAHJKAAPFL 240
FT	Modified-site	/note= "Asn is N-glycosylated"	Qy	1 MAARRRQRGRGEPTALLYPLAIGLGLALACIGLAVSLSRASLSAQEPQEEEL 60
FT	Modified-site	10 . 14	Db	1 MAARRRQRGRGEPTALLYPLAIGLGLALACIGLAVSLSRASLSAQEPQEEEL 60
FT	Peptide	/note= "amidation"	Qy	61 VAEEDDPSELNPOTSESQDAPFLNLRPERSAKGRKTRARIAAHYEVHPRPGQD 120
FT	Peptide	97 . 101	Db	61 VAEEDDPSELNPOTSESQDAPFLNLRPERSAKGRKTRARIAAHYEVHPRPGQD 120
FT	Peptide	24 . 35	Qy	121 GAQAGVGDGTYSGWEEARINSSPLRNQIGEFIVTRAGLYYLQCQVHFDEGKAVYKLKD 180
XX	PN	/note= "prokaryotic membrane lipoprotein lipid"	RESULT 4	
XX	PN	WO200037638-A2.	AAU86129	
XX	PD	29-JUN-2000.	AAU86129 standard;	Protein; 249 AA.
XX	PP	02-DEC-1998; .	AAU86129;	
XX	PP	99WO-US28565.	AC	
Pr	Pr	22-DEC-1998; .	XX	
Pr	Pr	08-MAR-1999; .	DT	15-JUL-2002 (first entry)
Pr	Pr	98US-0113296.	XX	
Pr	Pr	99WO-US05038.	DE	Human PRO207 polypeptide.
Pr	Pr	0130432.	XX	
Pr	Pr	99US-0131445.	KW	Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
Pr	Pr	28-APR-1999; .	KW	leukaemia; neuronal disorder; stromal disorder; blastocoelic disorder;
Pr	Pr	99US-0134287.	KW	inflammatory disorder; immune disorder; angiogenic disorder;
Pr	Pr	14-MAY-1999; .	KW	cytostatic; neuroprotective.
Pr	Pr	99US-0134428.	XX	
Pr	Pr	26-JUL-1999; .	OS	Homo sapiens.
Pr	Pr	99US-0144758.	XX	
Pr	Pr	15-SEP-1999; .	PN	WO200153486-A1.
Pr	Pr	99WO-US21090.	XX	
Pr	Pr	15-SEP-1999; .	PD	26-JUL-2001.
Pr	Pr	99WO-US21547.	XX	
XX	PA	(GETH) GENENTECH INC.	PP	11-FEB-2000; 2000WO-US05565.
XX	PA	PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Marsters SA;	XX	
PI	PI	PI Napier MA, Pitti RM, Wood WI;	DR	08-MAR-1999; 99WO-US05028.
PI	PI	WPI: 2000-442668/38.	PR	11-MAR-1999; 99US-123972P.
DR	DR	N-PSDB; AA449717.	PR	11-MAY-1999; 99US-133459P.
XX	PT	Novel composition to inhibit neoplastic cell growth or for treating	PR	02-JUN-1999; 99WO-US12252.
PT	PT	tumor in mammal comprises polypeptides PRO179, PRO207, PRO320, PRO219,	PR	22-JUN-1999; 99US-140650P.
PT	PT	PT PRO222, PRO224, PRO328, PRO362, PRO356, PRO59 or	PR	22-JUL-1999; 99US-140653P.
PT	PT	PRO866 .	PR	20-JUL-1999; 99US-144758P.
XX	PS	Claim 19; Fig 4; 172pp; English.	PR	28-JUL-1999; 99US-146222P.
PS	PS	XX	PR	17-ANG-1999; 99US-149395P.
XX	CC	The present sequence is that of human antitumour protein PRO207,	PR	31-AUG-1999; 99US-151689P.
CC	CC	as deduced from a fetal kidney cDNA clone (see AKA971). PRO207	PR	01-SEP-1999; 99WO-US2011.
CC	CC	shows amino acid sequence identity to tumour necrosis factor family	PR	15-SEP-1999; 99WO-US21090.
CC	CC	members, especially human lymphotoxin-beta (23.4%) and human	PR	30-NOV-1999; 99WO-US28113.
CC	CC	ligand (19.8%). Mol wt. is 27,216. A claimed method for inhibiting	PR	01-DIC-1999; 99WO-US28301.
CC	CC	the growth of a tumour cell comprises exposing the tumor cell	PR	01-DEC-1999; 99WO-US28634.
CC	CC	to PRO179, PRO207, PRO221, PRO224, PRO328, PRO301,	PR	05-JAN-2000; 2000WO-US00219.
CC	CC	PRO226, PRO362, PRO366, PRO59 or PRO66 (see AAY5337-49), their	XX	(GETH) GENENTECH INC.
CC	CC	agonists or chimeric polypeptides incorporating them. The tumour	PI	Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillian KJ,
CC	CC	is especially a cancer selected from breast, ovarian, renal,	PI	Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;
CC	CC	colorectal, uterine, prostate, lung, bladder and central nervous	PI	Watanabe CK, Wood WI;
CC	CC	system cancer, melanoma and leukaemia. Methods for the recombinant	XX	WPI: 2002-205567/26.
CC	CC	expression of the antitumour proteins are also provided.	DR	N-PSDB; ABK40255.
XX	SQ	Sequence 249 AA;	XX	XX
Qy	Qy	Best Local Similarity 100.0%; Score 1268; DB 21; Length 249;	PT	Thirteen five nucleic acids encoding PRO polypeptides, useful for
Qy	Qy	Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	PT	treating benign or malignant tumours, leukaemias and lymphoid
Db	Db	1 MAARRRQRGRGEPTALLYPLAIGLGLALACIGLAVSLSRASLSAQEPQEEEL 60	PT	malignancies, inflammations, angiogenic and immunologic disorders -
Db	Db	1 MAARRRQRGRGEPTALLYPLAIGLGLALACIGLAVSLSRASLSAQEPQEEEL 60	PS	Claim 61; Fig 4; 302pp; English.
Qy	Qy	61 VAEEDDPSELNPOTSESQDAPFLNLRPERSAKGRKTRARIAAHYEVHPRPGQD 120	XX	The present invention relates to the isolation of novel human PRO
Db	Db	61 VAEEDDPSELNPOTSESQDAPFLNLRPERSAKGRKTRARIAAHYEVHPRPGQD 120	CC	polypeptides and the polynucleotide sequences encoding them. The
Qy	Qy	121 GAQAGVGDGTYSGWEEARINSSPLRNQIGEFIVTRAGLYYLQCQVHFDEGKAVYKLKD 180	CC	PRO polypeptides, agonists, antagonists or anti-PRO antibodies are

macrophagal, stromal and blastocoelic disorders, inflammatory, immune and angiogenic disorders. The polynucleotide sequences are also useful in gene therapy. AAU86128-AAU86162 represent the human PRO polypeptides of the invention.

macrophagal stromal and blastocoelic disorders, inflammatory, immune and angiogenic disorders. The polynucleotide sequences are also useful in gene therapy. AAU86128-AAU86162 represent the human PRO polypeptides of the invention.

WPI: 1998-447255/38.
N-PSDB; AAV7613.
Detecting nucleic acid encoding TREPA - useful for diagnosis and treatment of autoimmune disease, tumours and inflammation

Sequence	249 AA;	Query Match	99.81;	Score	1265;	DB	119;	Length	249;
	Best Local Similarity	99.61;	Pred.	No. 2	8.e-13;				
	Matches	248;	Conservative	1;	Minmatches	0;	Indels	0;	Gaps
									0;
1	MAARRSORRGRGEPTOTALLYPLAIGLGLALAIGLGLLAVALSGRASISQAQEPAQEEL	60							
1	MAARRSOKRGRGEPTOTALLYPLAIGLGLALAIGLGLLAVALSGRASISQAQEPAQEEL	60							
61	VAEEDQDPSLEINPQTEESQDPAFPFLNRLVRPRSPASKGRKTRARRAIAAHYEVHPRPGOD	120							
61	VAEEDQDPSLEINPQTEESQDPAFPFLNRLVRPRSPASKGRKTRARRAIAAHYEVHPRPGOD	120							
121	GAQAGYDGTYSGWEEARINSSSPLYRNQIGEFTIVTRAGLYYLQCOYHFEDEGKAVYLKL	180							
121	GAQAGYDGTYSGWEEARINSSSPLYRNQIGEFTIVTRAGLYYLQCOYHFEDEGKAVYLKL	180							
181	LLVGVYLALRCLLEFSATAASSLGQPLRLCQVSGLLALRPSSLIRTLPAHLKAAPFL	240							
181	LLVGVYLALRCLLEFSATAASSLGQPLRLCQVSGLLALRPSSLIRTLPAHLKAAPFL	240							
241	TYFGFLFQVH	249							
241	TYFGFLFQVH	249							

EE00891	AAE00891 standard; Protein; 249 AA.	
AAE00891;		
	04-JUL-2001 (first entry)	
	Human TREPA (TNF related endothelium proliferative agent).	
	Human; tumour necrosis factor; TNF; angiogenesis; wound healing; TREPA; TNF related endothelium proliferative agent; tumour; metastasis; grafting; vulnery.	
	HOMO sapiens.	
	Key Domain	Location/Qualifiers
		9A 249

EE00891 AAE0

0891;

RESULT 8

AAU03499 ID AAU03499 Standard; Protein; 273 AA.

卷之三

AC AAU03499;

Key	Location/Qualifiers
Domain	98 249
Homo sapiens.	
INF	related endothelium proliferative agent; tumour; metastasis; grafting; vulnerability.

KW	preneoplastic condition; myocardial angiogenesis; wound granulation
KW	scleroderma; vascular adhesion; telangiectasia; ischaemia; human;
KW	atherosclerotic plaque neovascularisation; coronary atherosclerosis;
KW	peripheral atherosclerosis; pdc409-12-TWEAK; TWEAK receptor; TWEAK fusion protein.
OS	
OS	Homo sapiens.
OS	Synthetic.
SPN	WO200145730-A2.
XX	
XX	28-JUN-2001.
PD	
XXX	19-DEC-2000; 2000WO-US34755.
PPF	
XXX	20-DEC-1999; 99US-0172878.
PR	
PR	10-MAY-2000; 2000US-0203347.
PA	
PA	(IMMUNEX CORP.
XX	
XX	Wiley SR;
PS	
XX	Example 1; Page 41; 46pp; English.
XX	
DR	
DR	WPI: 2001-417975/44.
DR	N-PSDB; ASN03964.
XX	
PPT	
PPT	Modulating angiogenesis in a mammal for treating diseases mediated by
PPT	angiogenesis, e.g. solid tumours and vascular deficiencies of cardiac
PPT	peripheral tissue, by administering antagonist or agonist of TWEAK
PPT	receptor
XX	
PS	
XX	The sequence represents a fusion protein encoded by the
CC	expression vector pdc409-12-TWEAK. The fusion protein comprises a
CC	growth hormone leader, a leucine zipper multimerisation domain, and
CC	the extracellular domain of human TWEAK. The fusion protein was
CC	used in the isolation of human TWEAK receptor (TWEAK) -expressing
CC	clones from a COS cell human cDNA library. The TWEAK protein is
CC	a member of the tumour necrosis factor (TNF) family and induces
CC	angiogenesis. TWEAK may therefore be used to screen for and
CC	develop TWEAK agonists and antagonists for the modulation of
CC	angiogenesis, to be used in the treatment and diagnosis of human diseases
CC	mediated by angiogenesis include ocular disorders
CC	characterised by ocular neovascularisation such as diabetic retinopathy,
CC	neovascular glaucoma, retinoblastoma, retinopathy of prematurity, and
CC	retrolental fibroplasia, rubesis, uveitis, macular degeneration, and
CC	corneal graft neovascularisation, and inflammatory diseases such as
CC	arthritis, rheumatism and psoriasis. Other treatable diseases include
CC	malignant and metastatic conditions such as sarcomas and carcinomas,
CC	benign tumours and preneoplastic conditions, myocardial angiogenesis,
CC	haemophilic joints, scleroderma, vascular adhesions, atherosclerotic
CC	plaque neovascularisation, telangiectasia, wound granulation, corona-
CC	atherosclerosis, peripheral atherosclerosis and ischaemia.
XX	
SQ	Sequence 273 AA;
	Query Match 84.1%; Score 1066; DB 22; Length 273;
	Best Local Similarity 100.0%; Pred. No. 4e-99;
	Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	
Db	
43	SLGSASLSDAQPQQELVAEEDQPSLNPQTESDQPAFLNRLPSPRNLVPRRSAFKGRKTR
67	SLGSASLSDAQPQQELVAEEDQPSLNPQTESDQPAFLNRLPSPRNLVPRRSAFKGRKTR
Qy	
Db	
103	ARRAAAHYEVHPRPGDGAQGVDTGTVSGWEARINSSSPLYRQIGEFTIVTRAGLYY
127	ARRAAAHYEVHPRPGDGAQGVDTGTVSGWEARINSSSPLYRQIGEFTIVTRAGLYY
Qy	
Db	
163	LYCQHFDEGKAVYLKIDLLVDPGLYALRCLEESATAASSLGPQLRCVSGSLALRPGS
167	LYCQHFDEGKAVYLKIDLLVDPGLYALRCLEESATAASSLGPQLRCVSGSLALRPGS
Qy	
Db	
223	SLRIRTLPWHLKAAPPLTYFGLFQVH 249

Db	247	SLRIRTLPAWHLKAAPFLTYFGFQVH	273
RESULT 9			
	AAW93590	AAW93590 standard; Protein;	208 AA.
ID	AAW93590		
XX	XX	Tumour necrosis factor receptor; sign	
KW	KW	developmental abnormality; gestation	
AC	AC	APO6; APO8; TNRL-1; TNRL-3; di	
XX	XX	Cytoplasmic domain; immunogen; auti	
DT	18-JUN-1999	apoptosis; human.	
XX	XX		
DE	Human TNRL3 protein.		
XX	XX		
KW	KW		
AC	AC		
XX	XX		
OS	Homo sapiens.		
XX	XX		
BN	W09911791-A2.		
XX	XX		
PD	PD		
XX	11-MAR-1999.		
PF	PF		
XX	98WO-US18393.		
PR	PR		
XX	04-SEP-1998;		
PR	PR		
XX	05-SEP-1997;		
PA	PA		
XX	97US-0924634.		
PAW	(UNIW) UNIV WASHINGTON.		
PI	PI		
XX	Chaudhary PM;		
DR	WPI; 1999-205191/17.		
DR	N-PSDB; A0X23424.		
XX	XX		
PT	New Tumor Necrosis Factor family rec		
PT	PT		
PR	useful for diagnosis and treatment o		
PR	PR		
XX	developmental or gestational abnorma		
PS	PS		
XX	Claim 40; Fig 13A: 156pp; English.		
CC	This invention describes isolated tu		
CC	mer necrosis factor receptor polypeptides: APO4, APO6. A		
CC	fragments, and isolated TNF related		
CC	their active fragments. APO4 is used		
CC	to determine levels of APO4 in an		
CC	be treated using APO4 selective bind		
CC	moeity. APO4 polypeptides are also u		
CC	binding agents, useful in diagnosis/		
CC	agents to the polypeptide/active fra		
CC	expressed on the cell surface. The b		
CC	vivo. APO4 Polypeptides/ active frag		
CC	for agonists and antagonists by bind		
CC	activity. Effective pharmacological		
CC	treatment of disease are also identi		
CC	fragments and APO4 signal transducer		
CC	with a cytoplasmic domain of APO4 an		
CC	activity. The method is performed in		
CC	are all useful as immunogens for pre		
CC	useful for diagnosis/treatment of de		
CC	abnormalities. APO8 was transfected		
CC	MCF-7, and induced apoptosis.		
XX	XX		
SQ	Sequence 208 AA;		
XX	XX		
Query	Match	83.8%	Score
Best	Local Similarity	99.5%	99.5%
Matches	Matches 207;	Conservative	Pred. N
			0; Missm
42	VSLSGRASLSAQEPAAQELVAAEDQDPSLN		

Db 1 VSLGRASLQAQEPQELVAVEDQDPSELNPOTEESQDPAPFLNRLVRPRSAAPKGRKT 60
 Qy 102 RARRAIAHYEYHPRPGDQAQGVDRGSGMEARINSSPQRNQIGETIVTARGLY 161
 Db 61 RARRAIAHYEYHPRPGDQAQGVDRGSGMEARINSSPQRNQIGETIVTARGLY 120
 Qy 162 YLYCQWHFDEGKAVYLKLDLIVDGVILARCLREFSATAASSLGPOIURLCOVSGLLALRPG 221
 Db 121 YLCQWHFDEGKAVYLKLDLIVDGVILARCLREFSATAASSLGPOIURLCOVSGLLALRPG 180
 Qy 222 SSRIRTLPWHLKAAPLTYFGLQVH 249
 Db 181 SSRIRTLPWHLKAAPLTYFGLQVH 208

RESULT 10
 AAW47524
 ID AAW47524 standard; Protein; 225 AA.
 Xv AAW47524;

Li 21-JUL-1998 (first entry)
 XX Mus musculus tumour necrosis factor related ligand (TRELL).
 XX Tumour necrosis factor related ligand; tnf; treatment;
 KW cancer; autoimmune disease; immune system; stimulation; suppression;
 KW graft rejection.
 XX Mus musculus.
 XX Key Location/Qualifiers
 PH 1..21 /note= "hydrophobic, transmembrane domain"
 FT Domain
 XX W09805783-A1.
 XX PD 12-FEB-1998.
 XX PF 07-AUG-1997; 97WO-US13945.
 XX PR 18-MAR-1996; 97US-0040820.
 PR 07-AUG-1996; 96US-0023541.
 PR 18-OCT-1996; 96US-0028515.
 XX PA (BIOJ) BIOPHARMA INC.
 PA (UYGE-) UNIV GENEVA FACULTY MEDICINE.

Browning JL, Chicheportiche Y;
 DR 1998-145619/13.
 DR N-PSDB; AAV18599.

AA DR
 PT Tumour necrosis factor related ligand - useful for, e.g. treating
 PT cancer, auto-immune disease and immune responses to tissue grafts
 XX Claim 12; Pages 48-50; 69pp; English.

PS The sequence is that of mouse tumour necrosis factor related
 CC ligand (TRELL). TRELL or active fragments can be included with a
 CC carrier in pharmaceutical compositions to treat cancer, autoimmune
 CC diseases or immune responses to tissue grafts, or to stimulate or
 CC suppress the immune system. It is useful to screen for TRELL or
 CC receptors, by labelling with a detectable label and screening
 CC compositions for binding. Agents interfering with TRELL-receptor
 CC can also be screened for, can then be administered,
 CC optionally with interferon- gamma, to induce cell death or
 CC treat, suppress or alter immune responses (especially involving human
 CC adenocarcinoma cells) involving a signal pathway between TRELL and its
 CC receptor. It's coding sequence can be used in gene therapy for
 CC TRELL-related disorders in mammals (especially humans), e.g. tumours,
 CC autoimmune and inflammatory diseases or inherited genetic disorders,
 CC by introducing into cells, and expressing, therapeutically effective

CC amounts of a vector, e.g. a virus comprising a gene encoding TRELL.
 CC It may also be of use in the preparation of prepare probes for
 CC screening natural/synthetic DNAs for TRELL-encoding sequences
 CC and for antisense therapy.

XX Sequence 225 AA;

Query Match 80.4%; Score 1020; DB 19; Length 225;
 Best Local Similarity 88.8%; Pred. No. 1.3e-14; Mismatches 16; Indels 0; Gaps 0;
 Matches 199; Conservative 9; Pairs 0;

Qy 26 LGGLALACLGLLAVSLSGRASLQAEPQELVADQDPSELNPOTEESQDPAPFL 85
 Db 2 LSGLGLALACLGLLVVLSGWSATLSAQESQELTAEDREPPENPOTEESQDVVPFL 61

Qy 86 NRLVRPRRSAPGKRKTRARRAIAHYEYHPRPGDQAQAGYDGTYSWEEARINSSPLR 145
 Db 62 EQLVRPRRSAPGKRKTRARRAIAHYEYHPRPGDQAQAGYDGTYSWEETKINNSPLR 121

Qy 146 YNRCQEFITVTRAGLYYLQCOVHDEGKAVYLKLDLIVDGVILARCLREFSATAASSLGP 205
 Db 122 YDRCQEFITVTRAGLYYLQCOVHDEGKAVYLKLDLIVDGVILARCLREFSATAASSLGP 181

Qy 206 QRLCQVSGLLARPSSLRITLPAHLKAAPLTYFGLQVH 249
 Db 182 QRLCQVSGLLPPLPQFSSLRITLPAHLKAAPLTYFGLQVH 225

RESULT 11
 AAB07527
 ID AAB07527 standard; protein; 225 AA.
 XX AAB07527;
 AC 20-OCT-2000 (first entry)
 DE Amino acid sequence of a soluble recombinant murine TWEAK protein.
 XX TWEAK protein; immunological disorder; immune response; inflammation;
 KW TWEAK blocking agent; autoimmune disease; organ transplant rejection;
 KW Graft-versus-Host disease; GVHD; lymphoid cell malignancy; shock; tumour.
 OS Mus sp.
 XX WO20042073-A1.
 PN 20-JUL-2000.
 XX 14-JAN-2000; 2000WO-US01044.
 XX 15-JAN-1998; 99US-0116168.
 XX (BIOJ) BIOPHARMA INC.
 PA XX
 PI Rennert P;
 XX DR WPI: 2000-476036/41.
 XX PT Preventing and treating immune responses using modulators, especially
 CC antibodies, of TWEAK, TWEAK receptors and TWEAK ligands, useful for
 PT treating e.g. inflammation and graft versus host disease.
 XX Disclosure; Fig 1; 45pp; English.
 CC The present sequence represents a TWEAK protein. The specification
 CC describes a method for preventing or treating an immunological
 CC disorder and/or inhibiting an immune response in an animal. The
 CC method comprises administering a TWEAK blocking agent. The method may
 CC be used for preventing and treating immune disorders associated with
 CC inappropriate expression and/or activity of TWEAK. These disorders
 CC include autoimmune diseases, acute and chronic inflammation, organ
 CC transplant rejection, Graft-versus-Host disease (GVHD), lymphoid cell
 CC malignancies, septic and other forms of shock, loss of immune

CC responsiveness (as seen in human immunodeficiency virus (HIV) infections) and failure of the immune response to tumour growth.

XX SQ Sequence 225 AA;

Query Match 80.4%; Score 1020; DB 21; Length 225;

Best Local Similarity 88.8%; Pred. No. 1.3e-94;

Matches 199; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

Qy 26 LGLGLALACGLLAVSLGSRASL-SAQEPQELVAEEDQDPSEIINPQTEESQDPAPEL 85

Db 26 LSLGLALACGLLAVSLGSRASL-SAQEPQELVAEEDQDPSEIINPQTEESQDPAPEL 61

Qy 86 NPLYPRRSAPKCRKTRARRAIAAHYETHPRCQDGAQAGUDGTGSGWEARINSSSSPLR 145

Db 62 EQLVPRRSAPKGRKARERRAIAAHYEVHPRCQDGAQAGUDGTGSGWEARINSSSSPLR 121

Qy 146 YNRQIGEFTVTRAGLYLQYQHFDGKAVYLKLDDLVGVIALRCLEEFSATAASSLGP 205

rh 122 YDRIQIGEFTVTRAGLYLQYQHFDGKAVYLKLDDLVGVIALRCLEEFSATAASSSPGP 181

206 QRLRCQVSGLLPLRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 249

Db 182 QRLRCQVSGLLPLRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 225

RESULT 13

AAW933591 ID AAW933591 standard; Protein; 211 AA.

XX AC AAW933591;

XX DT 18-JUN-1999 (first entry)

DE Mouse TNRL3 protein.

XX Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4; developmental abnormality; gestational abnormality; prostate; cancer; APO6; APO8; APO9; TNRL-1; INRL; diagnosis; treatment; therapy; disease; cytoplasmic domain; immunogen; antibody preparation; breast carcinoma; apoptosis; mouse.

OS Mus sp.

XX W00911791-A2.

XX PD 11-MAR-1999.

XX 04-SEP-1998; 98WO-US18393.

XX 05-SEP-1997; 97US-0324634.

XX DR N-PSDB; AAX23425.

XX PA (UNIW) UNIV WASHINGTON.

XX PI Chaudhary PM;

XX DR; 1997-205191/17.

XX PT New Tumor Necrosis Factor Family receptor polypeptides and ligands - useful for diagnosis and treatment of prostate cancer and developmental or gestational abnormalities

XX PS Claim 40; Fig 13B; 156pp; English.

XX This invention describes isolated Tumor Necrosis Factor (TNF) family receptor polypeptides: APO4, APO6, APO8 and APO9 or their active fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or their active fragments. APO4 is useful for diagnosing prostate cancer or by determining levels of APO4 in an individual. Prostate cancer can also be treated using APO4 selective binding agents linked to a therapeutic moiety. APO4 polypeptides are also useful for identifying selective binding agents, useful in diagnosis/treatment of disease by binding of

agents to the polypeptide/active fragment, which is extracellular, or expressed on the cell surface. The binding is preferably performed in vivo. APO4 polypeptides/ active fragments are also useful for screening for agonists and antagonists by binding and observing the change in APO4 activity. Effective pharmacological agent useful in diagnosis or treatment of disease are also identified using APO4 polypeptides/active fragments and APO4 signal transducer molecules that specifically interact with a cytoplasmic domain of APO4 and detecting a change in level of APO4 activity. The method is performed in vivo or in vitro. APO4 polypeptides are all useful as immunogens for preparing antibodies. APO4 is also useful for diagnosis/treatment of developmental or gestational abnormalities. APO8 was transfected to human breast carcinoma cell line MCF-7, and induced apoptosis.

XX SQ Sequence 211 AA;

Query Match 76.3%; Score 968; DB 20; Length 211;

Best Local Similarity 89.1%; Pred. No. 2.1e-89;

Matches 188; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

Qy 39 LAVVSLGSRASL-SAQEPQELVAEEDQDPSEIINPQTEESQDPAPELNLVPRRSAPKG 98

Db 1 LVVSLGSWATL-SAQEPQELVAEEDQDPSEIINPQTEESQDPAPELNLVPRRSAPKG 60

Qy 99 RTRARRAIAAHYEVHPRPGDGAQAGUDGTGSGWEARINSSPLRINQGEFATVRA 158

Db 61 RKRPRRAIAAHYEVHPRPGDGAQAGUDGTGSGWEETKNSSSPRLQYDQIGETVRA 120

Qy 159 GLYYLYCQVHFDGKAVYLKLDDLVGVIALRCLEEFSATAASSLGPQLCQVSGLLAL 218

Db 121 GLYYLYCQVHFDGKAVYLKLDDLVGVIALRCLEEFSATAASSSPQLRQLCQVSGLLAL 180

Qy 219 RGGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 249

Db 181 RGGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 211

RESULT 13

AAW29746 ID AAW29746 standard; Protein; 189 AA.

XX AC AAW29746;

XX DT 27-OCT-1998 (first entry)

XX DE TNF related endothelium proliferative agent protein 2.

XX KW TNF; endothelium proliferative agent; TREPA; wound healing; cancer; tissue grafting; vascularisation; apoptosis; autoimmune; birth control.

XX OS Homo sapiens.

XX WO9835061-A2.

XX PN WO9835061-A2.

XX PD 13-AUG-1998.

XX PP 12-FEB-1998; 98WO-US02859.

XX PR 10-FEB-1998; 98US-0021706.

XX PR 12-FEB-1997; 97US-07988692.

XX PA (ABBO) ABBOTT LAB.

XX PI Wiley SR;

XX DR; 1998-447255/38.

XX Detecting nucleic acid encoding TREPA - useful for diagnosis and treatment of autoimmune disease, tumours and inflammation

XX PS Claim 16; Page 125-6; 142pp; English.

CC The TNF-related endothelium proliferative agent (TREPA) , or its

protein - protein search, using sw model

on: April 12, 2003, 08:38:14 ; Search time 14 Seconds
(without alignments)
523.308 Million cell updates/

title: US-09-905-810-2
perfect score: 1268
sequence: 1 MAARSQRRGRGGEPGTAL..... PWAHLKAAPFLTYFGLFQVH 249
scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
reached: 262574 seqs, 29422922 residues
al number of hits satisfying chosen parameters: 262574

minimum DB seq length: 0
maximum DB seq length: 200000000
post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

database : Issued Patents_AA:
1: /cgns_6/_ptodata/1/iaa/5A_COMB_pep:
2: /cgns_6/_ptodata/1/iaa/5B_COMB_pep:
3: /cgns_6/_ptodata/1/iaa/6A_COMB_pep:
4: /cgns_6/_ptodata/1/iaa/6B_COMB_pep:
5: /cgns_6/_ptodata/1/iaa/PCRTS_COMB_pep:
6: /cgns_6/_ptodata/1/iaa/backfile61.pep:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being print and is derived by analysis of the total score distribution.

SUMMARIES

result	Query	Match	Length	DB	ID	Description
1	1265	99.8	249	4	US-09-105-343A-2	Sequence 2,
2	792	62.5	189	4	US-09-105-343A-3	Sequence 3,
3	761	60.0	146	4	US-09-105-343A-6	Sequence 6,
4	95.5	7.5	254	1	US-08-236-918A-4	Sequence 4,
5	95.5	7.5	254	4	US-09-150-866A-4	Sequence 4,
6	91.5	7.2	240	4	US-08-913-014A-1	Sequence 1,
7	91.5	7.2	240	4	US-09-072-993C-4	Sequence 4,
8	90	7.1	659	4	US-09-362-737-11	Sequence 11,
9	90	7.1	660	3	US-08-819-177-1	Sequence 11,
10	89	7.0	256	4	US-09-320-422-13	Sequence 13,
11	88.5	7.0	659	4	US-09-562-737-18	Sequence 18,
12	87	6.9	253	4	US-09-320-424-11	Sequence 11,
13	87	6.9	291	1	US-08-670-354-6	Sequence 6,
14	87	6.9	291	4	US-09-320-424-6	Sequence 6,
15	87	6.9	291	5	PCP-US52010995-6	Sequence 6,
16	86	6.8	1323	1	US-08-046-188E-4	Sequence 4,
17	85	6.7	294	3	US-08-996-133-11	Sequence 11,
18	85	6.7	294	4	US-08-995-689-11	Sequence 11,
19	85	6.7	294	4	US-09-215-619A-11	Sequence 11,
20	85	6.7	294	4	US-09-577-780-11	Sequence 11,
21	83.5	6.6	247	4	US-09-157-863-11	Sequence 4,
22	83.5	6.6	885	1	US-08-042-747A-8	Sequence 8,
23	83.5	6.6	885	3	US-08-804-433A-23	Sequence 23,
24	83.5	6.6	885	3	US-08-720-229-23	Sequence 23,
25	82	6.5	248	3	US-08-341-018-52	Sequence 52,
26	82	6.5	248	4	US-08-470-335-210	Sequence 210,
27	82	6.5	248	4	US-08-470-339-210	Sequence 210,

1 MARRSOKRRGRGECTALLYPLAGLGLALA**C**ILLAVS**S**ERASLSAQEPQEE 60
 Db 61 VAEEDDPSELNQTEESODPAPLNRLVRPRSA**D**KTRARRAAH**A**YEV**P**RGQD 120
 Qy 61 VAEEDDPSELNQTEESODPAPLNRLVRPRSA**D**KTRARRAAH**A**YEV**P**RGQD 120
 Db 121 GAQAGYDGTGVSGWEARINSSPLRNYRQIGEFIVTRAGLYC**Y**CCVH**F**DEGKAV**L**KLD 180
 Db 121 GAQAGYDGTGVSGWEARINSSPLRNYRQIGEFIVTRAGLYC**Y**CCVH**F**DEGKAV**L**KLD 180
 RESULT 3
 US-09-105-343A-6
 Sequence 6, Application US/09105343A
 Patent No. 6207642
 GENERAL INFORMATION:
 APPLICANT: WILEY, S. R.
 TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
 TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Abbott Laboratories
 STREET: 100 Abbott Park Road
 CITY: Abbott Park
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-6050
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows
 SOFTWARE: FastSEQ for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/105,343A
 FILING DATE: 12-FEB-1998
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US98/02859
 FILING DATE: 12-FEB-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: BECKER, Cherry L.
 REGISTRATION NUMBER: 35,441
 REFERENCE/DOCKET NUMBER: 6048.US.P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 847-935-1729
 TELEFAX: 847-938-2623
 TELEX:
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 146 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: No. 6207642e
 US-09-105-343A-6

Query Match 60.0%; Score 761; DB 4; Length 146;
 Best Local Similarity 100.0%; Pred. No. 1.e-69;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 RRAIAH**Y**EV**H**PR**G**Q**D**GA**Q**AG**D**GT**V**SG**W**EAR**I**NS**S**PLR**N**RQ**I**GE**F**IV**T**RL**G**LYL 163
 Db 1 RRAIAH**Y**EV**H**PR**G**Q**D**GA**Q**AG**D**GT**V**SG**W**EAR**I**NS**S**PLR**N**RQ**I**GE**F**IV**T**RL**G**LYL 60
 Qy 164 Y**C**Q**Y**H**F**DE**G**KAV**L**KLD**I**LV**D**G**V**LA**R**CL**E**EF**A**ASS**L**GP**O**URL**C**V**S**GL**L**AL**R**PG**S** 223
 Db 61 Y**C**Q**Y**H**F**DE**G**KAV**L**KLD**I**LV**D**G**V**LA**R**CL**E**EF**A**ASS**L**GP**O**URL**C**V**S**GL**L**AL**R**PG**S** 120
 Qy 224 LR**I**RT**L**PM**A**HL**K**A**P**EL**T**Y**F**GL**Q**V**H** 249
 Db 121 LR**I**RT**L**PM**A**HL**K**A**P**EL**T**Y**F**GL**Q**V**H** 146
 RESULT 4
 US-08-236-918A-4

Query Match 62.5%; Score 792; DB 4; Length 189;
 Best Local Similarity 99.3%; Pred. No. 1.e-72;
 Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 97 KGRKTRARRA**A**HH**Y**EV**H**PR**G**Q**D**GA**Q**AG**D**GT**V**SG**W**EAR**I**NS**S**PLR**N**RQ**I**GE**F**IVT 156
 Db 37 KGRKTRARRG**A**HH**Y**EV**H**PR**G**Q**D**GA**Q**AG**D**GT**V**SG**W**EAR**I**NS**S**PLR**N**RQ**I**GE**F**IVT 96

Sequence 4, Application US/08236918A
 Patent No. 5614704
 GENERAL INFORMATION:
 APPLICANT: Alderson, Mark R.
 COMPUTER: Goodwin, Raymond G.
 TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand and Human Receptor
 NUMBER OF SEQUENCES: 18
 CORTINER ADDRESS: Cytokine Designated 4-1BB Ligand
 ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: Washington
 COUNTRY: US
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Power Macintosh
 OPERATING SYSTEM: Apple 7.5.3
 SOFTWARE: Microsoft Word, Version #6.0.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/216,918A
 FILING DATE: 06-May-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/060,843
 FILING DATE: 07-May-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Anderson, Kathryn A.
 REGISTRATION NUMBER: 32,172
 REFERENCE/DOCKET NUMBER: 2801-B
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 231-0644
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 254 amino acids
 TOPOLGY: linear
 MOLECULE TYPE: protein
 US-08-236-918A-4

Query Match 7.5%; Score 95.5; DB 1; Length 254;
 Best Local Similarity 25.7%; Pred. No. 0.075; Indels 73; Gaps 11;
 Matches 66; Conservative 31; Mismatches 87; Indels 73; Gaps 11;
 Query Match 7.5%; Score 95.5; DB 4; Length 254;
 Best Local Similarity 25.7%; Pred. No. 0.075; Indels 73; Gaps 11;
 Matches 66; Conservative 31; Mismatches 87; Indels 73; Gaps 11;
 Qy 19 ALLVPLAIGLGLALACGLLAVSL-GSRASL-SAQEPQELVAEEQDPSLEINPQTE 76
 Db 30 ALVAGLILLLAAGAACAVFLACPWAVSGARASPSAASPRLE-----GPELSP--- 78
 Qy 77 ESQDPAPFLNRLVRPRRSAPKGKTRARRAIAAHYEVHPRPGDGAQAGDGTGTVGWE- 135
 Db 79 -DDPAGLLDL-----RQGMPAQLVQANVLL-----IDGPLSWYSDP 113
 Qy 136 --ARINSSSPLYNRQIGEFIVTRAGLYLYCQVHDFEGKAVYLKDLVVDG-----VL 187
 Db 114 GLAGYSLTGSLSYKETKELVAKAGVYVFFQ-----LIALRPGSSLRIRTLPWAHLK 235
 Qy 188 ALRCLEFSATAASSLGQQLRCQVSG-----LIALRPGSSLRIRTLPWAHLK 235
 Db 164 ALHQQLPLRSAAGAAALALTVDLPASSEARNSAFQGQRLLHSAGQRLGHLTEARAR 223
 Qy 236 AAPFL---TYFGLFQV 248
 Db 224 HAWQLTQGATVGLGLFRV 240

RESULT 6
 US-08-913-014A-1
 Sequence 1, Application US/08913014A
 Patent No. 6235878
 GENERAL INFORMATION:
 APPLICANT: Nishi, Kazunori
 APPLICANT: Hikichi, Yukiko
 APPLICANT: Shintani, Yasushi
 TITLE OF INVENTION: NOVEL 4-1BB-LIKE PROTEIN, ITS
 TITLE OF INVENTION: PRODUCTION AND USE
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David G. Conlin, Esq.
 STREET: 130 Water Street
 CITY: Boston,
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/913,014A
 FILING DATE: 04-SEP-1997
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP97/02480

RESULT 5
 US-09-150-864A-4
 Sequence 4, Application US/09150864A
 Patent No. 6355779
 GENERAL INFORMATION:
 APPLICANT: Alderson, Mark R.
 COMPUTER: Goodwin, Raymond G.
 TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand and Human Receptor
 NUMBER OF SEQUENCES: 18
 CORTINER ADDRESS: That Binds Thereto
 ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: Washington
 COUNTRY: US
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/913,014A
 FILING DATE: 04-SEP-1997
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP97/02480

REGISTRATION NUMBER: 32,983
 REFERENCE/DOCKET NUMBER: 07917/037001
 TELEPHONE: 617-542-5070
 TELEFAX: 617-542-8306
 SEQUENCE CHARACTERISTICS:
 LENGTH: 660 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 FEATURE:
 OTHER INFORMATION: JIP-1 protein

Query Match 7.1%; Score 90; DB 3; Length 660;
 Best Local Similarity 26.5%; Pred. No. 1;
 Matches 40; Conservative 16; Mismatches 59; Indels 36; Gaps 6;

29 IGLALAC--LGL--LLAVVLSGRASRSLAQEAQEEV----NEEQDQ----
 Db 56 GISLQCKDTLSLRPAGLSSGSSAGSLQOAEMLQMDLIDAAGDTPGAEDDEBEDD 115

Qy 68 -----PSELNPQTEESQDPAPFLNRLVRPRRSAP--KGKRTRARRAIAAHYEVHPRPG 118

Db 116 ELAAQPGVPGVGPRAESQQDPA-----RSQGQPGTGSQDTYRPRPTTUNLFPPVPRS 169

Qy 119 QDGQAQGVGDGTVSGWEEARINGSSSPLYNRQ 149

Db 170 QDTLNNSLGIKHSWQDRVRSSSSPKRTGEQ 200

RESULT 10
 US-09-320-424-13
 Sequence 13, Application US/09320424
 Patent No. 6284236
 GENERAL INFORMATION:
 APPLICANT: Wiley, Steven R.
 APPLICANT: Goodwin, Raymond G.
 TITLE OF INVENTION: Cytokine that Induces Apoptosis
 FILE REFERENCE: 2835-E
 CURRENT APPLICATION NUMBER: US/09/320,424
 CURRENT FILING DATE: 1999-05-26
 EARLIER APPLICATION NUMBER: 09/190,046
 EARLIER FILING DATE: 1998-11-10
 EARLIER APPLICATION NUMBER: 09/048,641
 EARLIER FILING DATE: 1999-03-26
 EARLIER APPLICATION NUMBER: 08/670,354
 EARLIER FILING DATE: 1996-06-25
 EARLIER APPLICATION NUMBER: 08/548,368
 EARLIER FILING DATE: 1995-11-01
 EARLIER APPLICATION NUMBER: 08/496,632
 EARLIER FILING DATE: 1995-06-29
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 13
 LENGTH: 256
 TYPE: PRT
 ORGANISM: Synthetic fusion

Query Match 7.0%; Score 89; DB 4; Length 256;
 Best Local Similarity 23.1%; Pred. No. 0.34;
 Matches 39; Conservative 25; Mismatches 67; Indels 38; Gaps 6;

28 IGLALACGLLIAVVGSGRSRSLASQPAQ-----ELVAAED 65
 Db 8 ISLLATLAVLAPLQSKRRTSSDMKQEDKAEILSKXHNEARIKJGERT 67

Qy 66 QDPSE--LNQPOTEESSQDPAPFLNRLVR--PRTSAPKGRKTRARRAIAAHYEVHPRPGQD 120
 Db 68 RSTSEETISTVQEQQNISP---LYVRGQRVAHITGTRGRSNTL-----SPNSK 117

Qy 121 GAQAGYDGTVSGWEEARINGSSSPLYNRQICEFIVTRAGLYLYCQVHF 169
 Db 118 NEKA-LGRKINSSRSRSGHFSLSNLHRLNGELVTHEKGFYIVSQTYF 165

RESULT 11
 US-09-562-737-18
 Sequence 18, Application US/09562737
 Patent No. 6428967
 GENERAL INFORMATION:
 APPLICANT: Herz, Joachim
 APPLICANT: Gotthardt, Michael
 TITLE OF INVENTION: LDL Receptor Signaling Pathways
 FILE REFERENCE: US580708
 CURRENT APPLICATION NUMBER: US/09/562,737
 CURRENT FILING DATE: 2000-05-01
 NUMBER OF SEQ ID NOS: 132
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 18
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Sequence

US-09-562-737-18

Query Match 7.0%; Score 88.5; DB 4; Length 659;
 Best Local Similarity 24.4%; Pred. No. 1.4;
 Matches 38; Conservative 18; Mismatches 57; Indels 43; Gaps 5;

Qy 18 TALLPLALGIGLAAACLGULLAVISLGSSASLSAQEPDDELVA-----BEDQD 67
 Db 64 TSLSLPPRAG-----LSSAASSSGASGRLLAEMLQMDLIMAAGDTPGAENDEEE 113

Qy 68 PSELNL-----POTEESDQPAFPFLNRLVRPRRSAPKGKRT-----RARRATAAHYEV 113
 Db 114 DDELQDQRPGVGPRAESNDPAP-----SSQGQGFCTGDTGSDTYRPRPTVNLFP 164

Qy 114 HPRPGDQAQAGVGDGTSGWEEARINGSSSPLYNRQ 149
 Db 165 QWPWSDTUNNNSYGRKHSMDRASRSSLKTDQ 200

RESULT 12
 US-09-320-424-11
 Sequence 11, Application US/09320424
 Patent No. 6284236
 GENERAL INFORMATION:
 APPLICANT: Wiley, Steven R.
 APPLICANT: Goodwin, Raymond G.
 TITLE OF INVENTION: Cytokine that Induces Apoptosis
 FILE REFERENCE: 2835-E
 CURRENT APPLICATION NUMBER: US/09/320,424
 CURRENT FILING DATE: 1999-05-26
 EARLIER APPLICATION NUMBER: 09/190,046
 EARLIER FILING DATE: 1998-11-10
 EARLIER APPLICATION NUMBER: 09/048,641
 EARLIER FILING DATE: 1999-03-26
 EARLIER APPLICATION NUMBER: 08/670,354
 EARLIER FILING DATE: 1996-06-25
 EARLIER APPLICATION NUMBER: 08/548,368
 EARLIER FILING DATE: 1995-11-01
 EARLIER APPLICATION NUMBER: 08/496,632
 EARLIER FILING DATE: 1995-06-29
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 11
 LENGTH: 253
 TYPE: PRT
 ORGANISM: Synthetic fusion

US-09-320-424-11

Query Match Score: 87; DB: 4; Length: 253;
 Best Local Similarity: 25.6%; Pred. No. 0 54;
 Matches: 30; Conservation: 22; Mismatches: 49; Indels: 16; Gaps: 5;
 RESULT 14
 US-09-320-424-6

Db 144 -ISKDGKTLG--QKIESWESSRKGHSLFLNHVLFRLNGELVIEQEGLYIYSQTYF 194

RESEQUENCE 6, Application US/09320424
 ; Sequence 6, Application US/09320424
 ; Patent No. 6384236
 ; GENERAL INFORMATION:
 ; APPLICANT: Wiley, Steven R.
 ; ATTORNEY/AGENT INFORMATION:
 ; APPLICANT: Goodwin, Raymond G.
 ; TITLE OF INVENTION: Cytokine that Induces Apoptosis
 ; FILE REFERENCE: 2835-E
 ; CURRENT APPLICATION NUMBER: US/09/320,424
 ; CURRENT FILING DATE: 1999-05-26
 ; EARLIER APPLICATION NUMBER: 09/190,046
 ; EARLIER FILING DATE: 1998-11-10
 ; EARLIER APPLICATION NUMBER: 09/048,641
 ; EARLIER FILING DATE: 1998-01-26
 ; EARLIER APPLICATION NUMBER: 08/670,354
 ; EARLIER FILING DATE: 1996-06-25
 ; EARLIER APPLICATION NUMBER: 08/548,358
 ; EARLIER FILING DATE: 1995-11-01
 ; EARLIER APPLICATION NUMBER: 08/496,632
 ; EARLIER FILING DATE: 1995-06-29
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 6
 ; LENGTH: 291
 ; TYPE: PRT
 ; ORGANISM: murine
 ; US-09-320-424-6

Query Match Score: 87; DB: 4; Length: 291;
 Best Local Similarity: 27.2%; Pred. No. 0 65; Mismatches: 16; Indels: 14; Gaps: 4;
 Matches: 31; Conservative: 16; Mismatches: 53; Indels: 14; Gaps: 4;
 Qy 58 EELVAEEDQDPSELNPQTEESQDPAPFLNRLVR--PRRSAPKGRKTRARRAIAAHYE 112
 Db 57 KKLIGEETRSTSETIISTVQEQRQNSIT---LVRERGPQRVAAHTGTRGRSNTS--- 109

Query Match Score: 87; DB: 1; Length: 291;
 Best Local Similarity: 27.2%; Pred. No. 0 65; Mismatches: 53; Indels: 14; Gaps: 4;
 Matches: 31; Conservative: 16; Mismatches: 53; Indels: 14; Gaps: 4;
 Qy 113 VHPRGQDGQAQGVDTGTVSGWBEARINSSPLRYNRQIGEFIVTRAGLYLYCQVHF 169
 Db 110 ---SPNSKNEKA-LGRKINSSWSSRSRSGHSFLSFLNHLRNGELVIEHERGFYYIYSQTYF 162

RESULT 15
 US-08-670-354-6

Query Match Score: 87; DB: 4; Length: 291;
 Best Local Similarity: 27.2%; Pred. No. 0 65; Mismatches: 16; Indels: 14; Gaps: 4;
 Matches: 31; Conservative: 16; Mismatches: 53; Indels: 14; Gaps: 4;
 Qy 58 EELVAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAP--KGRKTRARRAIAAHYEVHP 115
 Db 93 EETVLTRFQDTISTVQEQLSTPLP---RGGRPQKVAAHTGTRRSNSALIP----- 143

Query Match Score: 87; DB: 4; Length: 291;
 Best Local Similarity: 27.2%; Pred. No. 0 65; Mismatches: 16; Indels: 14; Gaps: 4;
 Matches: 31; Conservative: 16; Mismatches: 53; Indels: 14; Gaps: 4;
 Qy 116 RPQDGQAQGVDTGTVSGWEEARINSSPLRYNRQIGEFIVTRAGLYLYCQVHF 169
 Db 144 -ISKDGKTLG--QKIESWESSRKGHSLFLNHVLFRLNGELVIEQEGLYIYSQTYF 194

RESEQUENCE 6, Application PC/TUS9610895
 ; Sequence 6, Application PC/TUS9610895
 ; Patent No. 98101
 ; GENERAL INFORMATION:
 ; APPLICANT: Immunex Corporation
 ; ATTORNEY/AGENT INFORMATION:
 ; APPLICANT: Immunex Corporation
 ; TITLE OF INVENTION: Cytokine That Induces Apoptosis
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSSEE: Kathryn A. Anderson, Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Apple 7.5.2
 ; SOFTWARE: Microsoft Word, Version 6.0.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/670,354
 ; FILING DATE: 25-JUN-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/496,632
 ; FILING DATE: 29-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/548,368
 ; FILING DATE: 01-NOV-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Anderson, Kathryn A.
 ; REGISTRATION NUMBER: 32,172
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 587-0430
 ; TELEFAX: (206) 233-0644
 ; TELEX: 756822
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 291 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-670-354-6

Query Match Score: 87; DB: 1; Length: 291;
 Best Local Similarity: 27.2%; Pred. No. 0 65; Mismatches: 53; Indels: 14; Gaps: 4;
 Matches: 31; Conservative: 16; Mismatches: 53; Indels: 14; Gaps: 4;
 Qy 58 EELVAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAP--KGRKTRARRAIAAHYEVHP 115
 Db 92 EETVLTRFQDTISTVQEQLSTPLP---RGGRPQKVAAHTGTRRSNSALIP----- 143

Query Match Score: 87; DB: 1; Length: 291;
 Best Local Similarity: 27.2%; Pred. No. 0 65; Mismatches: 53; Indels: 14; Gaps: 4;
 Matches: 31; Conservative: 16; Mismatches: 53; Indels: 14; Gaps: 4;
 Qy 116 RPQDGQAQGVDTGTVSGWEEARINSSPLRYNRQIGEFIVTRAGLYLYCQVHF 169

APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756022
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10895-6

Very Match 6.9%; Score 87; DB 5; Length 291;
3st Local Similarity 27.2%; Pred. No. 0.65; Gaps 4;
Matches 31; Conservative 16; Mismatches 53; Indels 14; Gaps 4;
Matches 31; Conservative 16; Mismatches 53; Indels 14; Gaps 4;
Qy 58 EELVAEEDQDPSELNPQTEESQDPAPFLNRLYRPRRSAP--KGRKTRARRAIAAHYEVHP 115
Db 93 EETVLRTFQDTISTVPEKQKLSTPPLP--RGGRPQKVAAHITGITRSNSALP----- 143
Qy 116 RPGDQGAQAGVDTVSGWEARINSSPLRYNQIGEFIVTRAGLYYLYCQVHF 169
Db 144 -1SKDGKTLG--QKIESWESSRKGHSPLNHVLFRNGELVIEQEGLYTYSQTYF 194

Search completed: April 12, 2003, 08:39:40
Job time : 16 secs

Query Match	7.3% ; Score 93; DB 2; Length 378;	Best Local Similarity	25.6%; Pred. No. 3;	Matches	68; Conservation	C;Accession: S41710 R;Robert, P.R.; Coen, E.S.; Murphy, G.J.P.; Doonan, J.H. EMBO J. 13, 616-624, 1994 A;Title: Patterns of cell division revealed by transcriptional regulation of genes during cell division A;Reference number: S41709; MUID:94148000; PMID:8313906
Db	50 REGDRVVQGPIATLTLSSALEEGDSFAYLSR-----SAGQSSAAGSSRAATAQALAAE 104	Db	64 EIQDSEINPQTEESQDAPFNLNLVPRRS - A PKERKTRR-----RATAAHYEVHP 115	Db	105 SRQ-----LTQRAAALNRELAFAKRSLSAQTERTLTAAREYARAETIAAQGLSP 154	A;Status: nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-441 <P02> A;Cross-references: EMBL:X76123; NID:9425262; PIDN:CAA53729.1; PMID:9425263 C;Genetics: A;Gene: cyc2
Qy	116 RPGDGAQAGVGDGTSGMWEARINSSPLRYNRQIGEFLIVTRAGLYLYCQVHFDGKAV 175	Db	155 RE---LQARRDAELAVQEAESTLSSQALSYERQIGEY-----DARLA 193	Db	176 YLKLDL---LVDGVLAURCLEEFSATAASSLGPQLRLCQVSGSLA-----217	C;Superfamily: cyclin C;Keywords: cell cycle control; cell division control; mitosis
Db	194 AIPDQLQARAAFASTLQAGLQ-QATQVEAQGRYVVATVAGRAAALPVEAGQTGVGAA 252	Db	218 ---LRPQSSLRIRTLPWHLKAPFL 240	Db	253 VAVLTPGSDSALVAEL-YAPSRAFGV 277	C;Keywords: cell cycle control; cell division control; mitosis
RESULT 6						
A70611	hypothetical protein Rv1219c - Mycobacterium tuberculosis (strain H37RV)	Qy	91 PRRS---APKGKRTKARRATAAAHYEVHPRPGQ-----DGAQAGYDGTVSQWEE-----135	Db	139 GEBSLKKKAPPLTSTLTARTSAAASV-VRTKEKEQTIDADVNNDLAVVYVEDMYKFY 197	C;Species: Mycobacterium tuberculosis C;Accession: A70611 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998	A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.	Qy	136 -ARINSSSPLEY---NRCQIGEFLIVTRAGLYLYCQVHFD---EGKAVYKLKDLLYDGVL A 188	Db	198 RSAENDSRPHYMDQSPEINEKHM-RAILIDWLVQVHYKFELSPETLYLTIN-IVDRYLA 254	A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230 A;Status: Preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-212 <COL> A;Cross-references: GB:92316073; PIDN:92316073; PIDN:92316074 C;Genetics: A;Gene: Rv1219c
Qy	11 GRRGEPGTALLVPLAIGLGL---ALACLGHLAUVSLSGRASLASQEPQEEVAAE-- 64	Db	21 GRHG-----FVGVLRAIAEAAGVSAALVTHFGSKBGL---RKACDDFIAEIR 66	Db	65 -----DQDPSLENPQTERSDQDAPFLNLVPRRSAPKGRKTRARRAAHYEVHPR 116	C;Function: binds to the JNK protein kinase and inhibits JNK signal transduction pathway C;Species: Mus musculus (house mouse) C;Accession: T03038 R;Dickens, M.; Rogers, J.S.; Cavanagh, J.; Raitano, A.; Xia, Z.; Halpern, J.R.; Greenbaum, D.;Carrasco, R.; 693-696, 1997 Science 271, 693-696, 1997 A;Title: A cytoplasmic inhibitor of the JNK signal transduction pathway. A;Reference number: 214833; MUID:97382313; PMID:9235893 A;Accession: T03038 A;Status: Preliminary; translated from GB/EMBL/DBJ A;Molecule type: mRNA A;Residues: 1-66 <DCI> A;Cross-references: EMBL:AF003115; NID:92316073; PIDN:92316074 C;Genetics: A;Note: JIP-1
Db	67 SSSKAALKSNDPPTWLAQMATEIESTAPLMLVRSNQSGGFLAKMLWQKNI-----117	Db	68 -----PSEINPQTERSDQDAPFLNLVPRRSAPKGRKTRARRAAHYEVHPR 116	Db	69 -----GLALAC---LGL-----LIAVVLGSGRSRSLSAQEPQELV-----AEEOD-----67	A;Description: binds to the JNK protein kinase and inhibits JNK signal transduction pathway A;Function: binds to the JNK protein kinase and inhibits JNK signal transduction pathway A;Species: Mus musculus (house mouse) C;Accession: T03038 R;Dickens, M.; Rogers, J.S.; Cavanagh, J.; Raitano, A.; Xia, Z.; Halpern, J.R.; Greenbaum, D.;Carrasco, R.; 693-696, 1997 Science 271, 693-696, 1997 A;Title: A cytoplasmic inhibitor of the JNK signal transduction pathway. A;Reference number: 214833; MUID:97382313; PMID:9235893 A;Accession: T03038 A;Status: Preliminary; translated from GB/EMBL/DBJ A;Molecule type: mRNA A;Residues: 1-66 <DCI> A;Cross-references: EMBL:AF003115; NID:92316073; PIDN:92316074 C;Genetics: A;Note: JIP-1
Qy	117 PGQDGAQAGVGDGTSGMWEARINSSPLRYNRQIGEFLIVTRAGLYLYCQVHFD-----170	Db	118 ---DNAEFLY-----EGVRAGTVKPSRDRARARFLAIGGGFLYLQMHENPTDLR 168	Qy	119 QDGQAQAGVGDGTSGMWEARINSSPLRYNRQIGEFLIVTRAGLYLYCQVHFD-----170	C;Function: binds to the JNK protein kinase and inhibits JNK signal transduction pathway C;Species: Antirrhinum majus (garden snapdragon) C;Accession: S41710 C;Title: mitosis-specific cyclin 2 - garden snapdragon C;Reference number: S41710 C;Cross-references: EMBL:X76123; NID:9425262; PIDN:CAA53729.1; PMID:9425263 C;Genetics: A;Gene: cyc2 C;Keywords: cell cycle control; cell division control; mitosis
Db	171 -----EGKAYYLKUDLVLGVLAIRCL-EEFSATA 199	Db	169 AALRDIYAHDMVLPSSLEVYEGTLADRAMYEAFLEAA 204	Qy	120 -----PSEINPQTERSDQDAPFLNLVPRRSAPKGRKTRARRAAHYEVHPR 116	C;Function: binds to the JNK protein kinase and inhibits JNK signal transduction pathway C;Species: Antirrhinum majus (garden snapdragon) C;Accession: S41710 C;Title: mitosis-specific cyclin 2 - garden snapdragon C;Reference number: S41710 C;Cross-references: EMBL:X76123; NID:9425262; PIDN:CAA53729.1; PMID:9425263 C;Genetics: A;Gene: cyc2 C;Keywords: cell cycle control; cell division control; mitosis
RESULT 7						
S41710	mitosis-specific cyclin 2 - garden snapdragon	Db	116 ELAAORPGVGPCKAEQNQDAP-----RSQQGQGPCTGSGDTRPKRPTILNLFQVPRS 169	Qy	121 QDGQAQAGVGDGTSGMWEARINSSPLRYNRQ 149	C;Function: binds to the JNK protein kinase and inhibits JNK signal transduction pathway C;Species: Antirrhinum majus (garden snapdragon) C;Accession: S41710 C;Title: mitosis-specific cyclin 2 - garden snapdragon C;Reference number: S41710 C;Cross-references: EMBL:X76123; NID:9425262; PIDN:CAA53729.1; PMID:9425263 C;Genetics: A;Gene: cyc2 C;Keywords: cell cycle control; cell division control; mitosis

Db	189 HLLSPSSVFFGAF 202	Qy	18 TALLVPLALGLGLALACIGL-----LLAVVSLGSRASLISAQEPQ 57
RESULT 12			
D7045	hypothetical protein Rv0497 - Mycobacterium tuberculosis (strain H37RV)	Db	3 TALICALA-----ALCCUSTEQRKRDGVGSQVRVSHNESTHVNNGEDVTLCAHQHTS 57
C;Species: Mycobacterium tuberculosis	C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999	Qy	58 EELVAAE-----DODPSELNPQTEBSQ----DPAPFLNRLVRP---RRSA 95
C;Accession: D7045	R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 531-544, 1998	Db	58 ESVQQADITYYVERPENTVEYLRSURPFTGHSSHLSDLGPW---LIDDDDIWQSV 114
A;Authors: Squires, R.; Sulston, J. E.; Taylor, K.; Whitehead, S.; Barrell, B. G.	A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome	Qy	96 PKGRKTRAR----RAIAAHYEVHPR----PGDQGAQGVDTGTVSGMEARNTSSPLRYN 147
A;Reference number: A70500; MUID:88295987; PMID:9634220	A;Accession: D7045	Db	115 QRAHRSHTRLDOLILVQYMMGPEMTIPNHDSGHPL----THRMSA----- 160
A;Status: preliminary; nucleic acid sequence not shown; translation not shown	A;Molecule type: DNA	Qy	148 ROIGEFIVTR----AGIYLYCQVHFDEGKAVLKLDDLVGVLALRCLEFSATAASS 202
A;Cross-references: GB:Z7116; GB:AL123456; NID:93261606; PIDN: CAB00923.1; PID:e255036; A;Experimental source: strain H37RV	A;Genetics: Rv0497	Db	161 -EIGCWVILTRVTTDDVGTYVVFVVKPHNETAVATLRLDVLVRRPRVTVASAVFSATEDTC 219
RESULT 14			
B75346	probable competence protein ComBC/RecC - Deinococcus radiodurans (strain R1)	C;Species: Deinococcus radiodurans	
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000	C;Accession: B75346	R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Yamatnevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M. S.; Smith, H.O.; Ventris, J.C.; Fraser, C.M.	
Science 286, 1571-1577, 1999	A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.	A;Accession number: A75250; PMID:10567266	
A;Accession: B75346	A;Status: preliminary	A;Cross-references: GB:AE002025; MUID:20036896; PMID:96459627; PIDN:AAF11405.1; PID:964596	
A;Molecule type: DNA	A;Genetics: DR1854	A;Gene: DR1854	
RESULT 15			
Query Match 6 9%; Score 87; DB 2; Length 310;	Query Match 6.9%; Score 87; DB 2; Length 755;	Query Match 6.8%; Score 86.5; DB 2; Length 755;	RESULT 15
Best Local Similarity 24.0%; Pred. No. 7.6; Mismatches 90; Indels 114; Gaps 16;	Best Local Similarity 26.7%; Pred. No. 23; Mismatches 41; Indels 85; Gaps 10;	Best Local Similarity 26.7%; Pred. No. 23; Mismatches 41; Indels 85; Gaps 10;	B98121
Matches 72; Conservative 24; Mismatches 90; Indels 114; Gaps 16;	Matches 51; Conservative 14; Mismatches 41; Indels 85; Gaps 10;	Matches 51; Conservative 14; Mismatches 41; Indels 85; Gaps 10;	C;Species: Streptococcus pneumoniae
Qy 3 ARRSQRGG----RVEPPTGTAALVPLALGLGLALACIGLLLA 40	Db 80 -VQGEAAAPQSPAPVAQO-VAAEPTRTVWSQEPWPKSPQDPRRSQPELSEYRPL 137	Qy 8 RARRGRGEPG-TALLYPLAG-----LGLALAQLGL--LLAVVSL-44	C;Accession: E98121
Db 32 ARRRRRRDSDAITVAELTGEIPIIPIRDDHHAGDAAQSQAANGR-----79	Qy 93 R----SAPKGRKTRARRAI---AAHY-----EVHPRPGDGG-----121	Db 23 RRRGRHRAEAGRLAWPLALQPLAGIGGIGWQLGIGMAVPLLIGAALLDAPLLAVALL 82	R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; Dehoff, B. S.; Lee, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Y, P.; Sun, P.M.; Winkler, M.E.
Qy 41 VVSIGRSRSLAQPAQPEELVAEP-----DODPSELNPQTEESQDPAPFLNRLVRP 92	Db 138 RHTHSDRAGPQPGPQAEMSPDPVHEYDLDWTDVLDTEVGEAEATEVREAQFGRGERHA 197	Qy 45 -----GSRASLISAQEPQ-----BELYVNEEDQDPSELNPQTEESQDP 81	
Db 80 -VQGEAAAPQSPAPVAQO-VAAEPTRTVWSQEPWPKSPQDPRRSQPELSEYRPL 137	Qy 122 --AQAGVDGTVSGWEARINSSS---PLRYNHQIGEPIVTR-----AGLYLYCQV 167	Db 83 GGGLGIGS-AHQKQAREPDRTAAPWIGALVLTGRHWDQFLTIDEPKARVALAPKPRQGPGE 141	
Qy 168 HFDB---GKAYVLLKLDU----LVGDTGLALRCLEEFSAT-----AASSIGPQLRLCQ 211	Db 198 AAAAAGTVEGDDAEEAARRALDQVPTLWR---GALVVLQSLILAYAFAFGAIF----I 249	Qy 82 APFLNRLVRP---RR-----SAPKGRKTR-----RR 105	
Db 198 AAAAAGTVEGDDAEEAARRALDQVPTLWR---GALVVLQSLILAYAFAFGAIF----I 249	Qy 199 AFDQLWRWNNSIVALVLSSVWVILGLVVSVAVRKTEDIASTLIAVAGALITGP-LALLQ 308	Db 142 VVVAAGRJIRPGRJLPGGFDQAAWLRSQLGGILVTPKAVLWRAEVKKHVPERGLRGWFR 201	
RESULT 13			
T30604 hypothetical protein 3L - Molluscum contagiosum virus 1	Qy 166 AIAAHYEVHPR 116	Qy 106 AIAAHYEVHPR 116	
N;Alternative name: MC003L	Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210	
C;Species: Molluscum contagiosum virus 1	Qy 167 A;Status: preliminary; translated from GB/EMBL/DDBJ	Qy 167 A;Status: preliminary; translated from GB/EMBL/DDBJ	
C;Accession: T30604	A;Molecule type: DNA	A;Molecule type: DNA	
R;Senkovich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.	A;Residues: 1-445 <SEN>	A;Residues: 1-445 <SEN>	
Science 273, 813-816, 1996	C;Cross-references: EMBL:U60315; PIDN: AAC55131.1	C;Cross-references: EMBL:U60315; PIDN: AAC55131.1	
A;Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host re	A;Accession: T30604	A;Accession: T30604	
A;Reference number: 220876; MUID:96325459; PMID:8670425	A;Genetics: MC003L	A;Genetics: MC003L	
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Qy 168 HFDB---GKAYVLLKLDU----LVGDTGLALRCLEEFSAT-----AASSIGPQLRLCQ 211	Best Local Similarity 22.1%; Pred. No. 12; Mismatches 31; Indels 80; Gaps 12;	Best Local Similarity 22.1%; Pred. No. 12; Mismatches 31; Indels 80; Gaps 12;	Best Local Similarity 22.1%; Pred. No. 12; Mismatches 31; Indels 80; Gaps 12;
Db 198 AAAAAGTVEGDDAEEAARRALDQVPTLWR---GALVVLQSLILAYAFAFGAIF----I 249	Matches 56; Conservative 31; Mismatches 86; Indels 80; Gaps 12;	Matches 56; Conservative 31; Mismatches 86; Indels 80; Gaps 12;	Matches 56; Conservative 31; Mismatches 86; Indels 80; Gaps 12;
Qy 166 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116
Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210
Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116
Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210
Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116
Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210
Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116
Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210
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Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116
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Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116
Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210
Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116
Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210
Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116
Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210
Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116
Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210
Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116
Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210
Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116
Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210
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Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210
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Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210
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Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210	Db 202 GLSAH--LSPR 210
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Qy 167 AIAAHYEVHPR 116	Qy 167 AIAAHYEVHPR 116	Qy 167	

J. Bacteriol. 183, 5709-5717, 2001
 A; Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
 A; Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A; Reference number: A97872; MUID:21429245; PMID:11544234

A; Accession: E98121

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-762 <KUR>

A; Cross-references: GB:AE007317; PID:915459704; GSDB:CN00174

C; Genetics:

A; Gene: clpC-truncation

C; Superfamily: endopeptidase Clp ATP-binding chain

Query Match 6.8%; Score 86.5; DB 2; Length 762;

Best Local Similarity 23.4%; Pred. No. 23;

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Qy 42 VSLGSRASLQAQEPAGEELVAEEDDOPPSLNPQTEESQDPAPPFLNRLYRPRRSAP--KGR 99

Db 443 LSPADKALMDGKWKQOAAQJLAKEEBVYKRDLYVE--SDILTTUSRL---SGTPVQQLT 496

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Qy 100 KTRARRAIAAHYEVPRP-GDGAQAGVQDGTVSGWEARINSSSPRLYRNQIGFPI--- 154

~y ~y 100 KTRARRAIAAHYEVPRP-GDGAQAGVQDGTVSGWEARINSSSPRLYRNQIGFPI--- 154

Db 497 QTDKAKYLNIEAELHKRVIDQDQAVSSISRAI----RRNOSGTRSHRPIGSEMFILGP 550

Qy 155 --VTRAGLYYLYCQVHFDEGKAVYLRKLDLVDGTLALRCLEEEFATAASSLGPNURLCV 212

Db 551 TGVGKTELAKALAEVLFDESL-IRFDM-----SEYMEKFAASRLNGAPP----- 595

Qy 213 SGULALRPGSSL-RIRTLPWAH-----KAAP 238

Db 596 -GYGYEEGGELTEKVRNKEYSVLIFDEVKAHP 628

Search completed: April 12, 2003, 08:40:10

Job time : 26 secs

Result No.	Score	Query Match Length	DB ID	Description
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2	1020	80.4	225	TN12_MOUSE
3	109.5	8.6	272	TNFS_CHICK
4	108.5	8.6	260	TNFS_CANFA
5	95.5	7.5	201	TNFB_MACRF
6	95.5	7.5	254	TNFS_HUMAN
7	91.5	7.2	240	TN14_HUMAN
8	90	7.1	441	CG22_ANIMA
9	90	7.1	707	JIP1_MOUSE
10	87	6.9	197	TNFB_RABBIT
11	87	6.9	204	TNFB_BOVIN
12	87	6.9	291	TN10_MOUSE
13	87	6.9	310	Y497_MYCTU
14	86.5	6.8	250	TNFC_MACRF
15	86	6.8	139	YOFB_BACSU
16	86	6.8	205	TNFB_MARM
17	85	6.7	372	LMB_MOUSE
18	85	6.7	179	LMXB_HUMAN
19	84.5	6.7	933	VGLB_HSV21
20	84	6.6	310	TNFC_HSV20
21	83.5	6.6	885	VGLB_HSV25
22	83	6.5	228	B10D_PSEAB
23	83	6.5	936	FHL1_YEAST
24	82	6.5	288	RL2_ARATH
25	82	6.5	369	LMXB_MESU
26	82	6.5	844	PHSG_DROM
27	81.5	6.4	260	RL2_TOBAC
28	81.5	6.4	260	TNFS_FELCA
29	81	6.4	244	TNFS_BORBU
30	81	6.4	273	OSAS_BORBU
31	80.5	6.3	250	TN11_HUMAN
32	80.5	6.3	281	TN10_HUMAN
33	675	1	PRTS_BOVIN	

Scoring table:	BLOSUM62			
Gapop 10.0 , Gapext 0.5				
Searched:	112892 seqs, 41476328 residues			
at 1 number of hits satisfying chosen parameters:	112892			
Minimum DB seq length: 0				
Maximum DB seq length: 2000000000				
Post-processing: Minimum Match 0%				
Maximum Match 100%				
Listing First 45 Summaries				
Database :	SwissProt_40:*			
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES				
%				
Result No.	Query Score	Match Length	DB ID	Description
1	1268	100.0	249	TN12_HUMAN
2	1020	80.4	225	TN12_MOUSE
3	109.5	8.6	272	TNFS_CHICK
4	108.5	8.6	260	TNFS_CANFA
5	95.5	7.5	201	TNFB_MACRF
6	95.5	7.5	254	TNFS_HUMAN
7	91.5	7.2	240	TN14_HUMAN
8	90	7.1	441	CG22_ANIMA
9	90	7.1	707	JIP1_MOUSE
10	87	6.9	197	TNFB_RABBIT
11	87	6.9	204	TNFB_BOVIN
12	87	6.9	291	TN10_MOUSE
13	87	6.9	310	Y497_MYCTU
14	86.5	6.8	250	TNFC_MACRF
15	86	6.8	139	YOFB_BACSU
16	86	6.8	205	TNFB_MARM
17	85	6.7	372	LMB_MOUSE
18	85	6.7	179	LMXB_HUMAN
19	84.5	6.7	933	VGLB_HSV21
20	84	6.6	310	TNFC_HSV20
21	83.5	6.6	885	VGLB_HSV25
22	83	6.5	228	B10D_PSEAB
23	83	6.5	936	FHL1_YEAST
24	82	6.5	288	RL2_ARATH
25	82	6.5	369	LMXB_MESU
26	82	6.5	844	PHSG_DROM
27	81.5	6.4	260	RL2_TOBAC
28	81.5	6.4	260	TNFS_FELCA
29	81	6.4	244	TNFS_BORBU
30	81	6.4	273	OSAS_BORBU
31	80.5	6.3	250	TN11_HUMAN
32	80.5	6.3	281	TN10_HUMAN
33	675	1	PRTS_BOVIN	

ALIGNMENTS

RESULT 1

TN12_HUMAN

STANDARD;

PRT; 249 AA.

ID TN12_HUMAN

AC 043508; QBW027;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DE Tumor necrosis factor ligand superfamily member 12 (TNF-related weak inducer of apoptosis) (TNFAK) (APO3 ligand).

DN TNFS12 OR APO3 OR DR3LG

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Buthidae; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TaxID=9606;

RN

RP SEQUENCE FROM N.A., AND N-TERMINUS OF SOLUBLE FORM.

RC TISSUE-TONSL, and Fetal liver.

RX MEDLINE=98070415; PubMed=9405449;

RA Chicheportiche Y., Bourdon P.R., Xu H., Hsu Y.-M., Scott H., Hession C., Garcia I., Browning J.L.; Goddard A.,

RT "TWEAK, new secreted ligand in the tumor necrosis factor family that weakly induces apoptosis";

RL J. Biol. Chem. 272:32401-32410(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE-FETAL kidney;

RX MEDLINE=98228355; PubMed=9560343;

RA Marsters S., Sheridan J.P., Pitti R.M., Brush J., Goddard A., Ashkenazi A.;

RT "Identification of a ligand for the death-domain-containing receptor Apo3";

RL Curr. Biol. 8:525-528(1998).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE-TONSL;

RA Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

RN [4]

FUNCTION.

RN [5]

RP PubMED=10085077;

RA Lynch C.N., Wang Y.C., Lund J.K., Chen Y.-W., Wiley S.R.; "TWEAK induces angiogenesis and proliferation of endothelial cells.";

RL J. Biol. Chem. 274:8155-8159(1999).

CC -!- FUNCTION: Binds to TNF14 and possibly also to TNRFS12/APO3. Weak inducer of apoptosis in some cell types. Mediates NF-KappaB activation. May promote angiogenesis and the proliferation of endothelial cells.

CC -!- SUBUNIT: HOMOTRIMER (POTENTIAL).

CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted.

CC -!- TISSUE SPECIFICITY: Highly expressed in adult heart, pancreas, skeletal muscle, brain, colon, small intestine, lung, ovary, prostate, spleen, lymph node, appendix and peripheral blood lymphocytes. Low expression in kidney, testis, liver, placenta, thymus and bone marrow. Also detected in fetal kidney, liver, lung and brain.

CC -!- PRM: The soluble form derives from the membrane form

CC by proteolytic processing. BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -!- SIMILARITY: Ref.3 sequence differs from that shown due to a
 CC frameshift in position 125.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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 CC or send an email to license@isb-sib.ch).

CC

DR EMBL; AF03009; AAC51923; 1; -;

DR EMBL; AF055872; AAC39724; 1; -;

DR EMBL; BC019047; AAC119047; 1; ALT_FRAME.

DR Genew; HGNC:11927; TNFSF12.

DR InterPro; IPI000418; TNF_1.

DR PTan; PF00229; TNF_1.

DR SMART; SM00207; TNF_1.

DR PROSITE; PS00251; TNF_1; FALSE_NEG.

DR PROSITE; PS50049; TNF_2; 1.

DR Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.

KW

FT CHAIN 1 249 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 12, MEMBRANE FORM.

FT CHAIN 94 249 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 12, SECRETED FORM.

FT DOMAIN 1 21 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 22 42 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL)..

FT DOMAIN 43 249 EXTRACELLULAR (POTENTIAL).

FT SITE 93 94 CLEAVAGE.

FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .).

SQ SEQUENCE 249 AA; 27216 MN; E66084336128BEA CRC64;

Query Match Best local Similarity 100.0%; Score 1268; DB 1; Length 249; Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAARSQRGRRGRREPGRTALLPVALGLALCGLLAVSIGSRLSQAQPQEL 60

Db 1 MAARSQRGRRGRREPGRTALLPVALGLALCGLLAVSIGSRLSQAQPQEL 60

Qy 61 VAEDDQDPSELNPQTEESDOPAPLNRLVPRASAPGRKTRARRATAHYEYPRPQD 120

Db 61 VAEDDQDPSELNPQTEESDOPAPLNRLVPRASAPGRKTRARRATAHYEYPRPGD 120

Qy 121 GAQPGVGDGTIVSGWREARINSSPRYRNQIGEFIVTRAGLYLICQVHFDEGRAVYLKD 180

Y 121 GAQPGVGDGTIVSGWREARINSSPRYRNQIGEFIVTRAGLYLICQVHFDEGRAVYLKD 180

Db 121 GAQPGVGDGTIVSGWREARINSSPRYRNQIGEFIVTRAGLYLICQVHFDEGRAVYLKD 180

Qy 181 LLVVGVLALRCLEFSATASSLCPQLRLCQVSSLALRGSSSRIRTLPWAKKAAPFL 240

Db 181 LLVVGVLALRCLEFSATASSLCPQLRLCQVSSLALRGSSSRIRTLPWAKKAAPFL 240

Qy 241 TYFLGFQVH 249

Db 241 TYFLGFQVH 249

RESULT 2

ID TN12_MOUSE STANDARD; PRT; 225 AA.

AC 05427; 09CTP2;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Tumor necrosis factor ligand superfamily member 12 (TNF-related weak inducer of apoptosis) (TWEAK) (Fragment).

GN TNFF12

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

FT	DISU1:PTD	167	186	POTENTIAL, N-LINKED (GLCNAC, .) (POTENTIAL).	DR	PROSITE; PS00251; TNF 1; 1;	
FT	CARBOHYD	115	115	N-LINKED (GLCNAC, .) (POTENTIAL).	DR	PROSITE; PS00044; TNF 2; 1;	
SQ	SEQUENCE	225	AA;	24781 MW; 90C412C040659B CRC64;	KW	Cytokine; Transmembrane; Glycoprotein; Signal-anchor.	
Query Match	Best Local Similarity	80.4%	Score 1020;	DB 1;	FT	TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 5, MEMBRANE FORM.	
Matches 199;	Conservative	88.8%	Pred. No. 1.1e-78;	Length 225;	FT	TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 5, SOLUBLE FORM (BY SIMILARITY).	
Qy	26	LSLGLALACGLLAVSLGSASLSAQEPQELVAEQQDSEINPQTEESQDPAPFL 85	FT	DOMAIN 1	FT	CYTOSPLASMIC (POTENTIAL) SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).	
Db	2	LSLGLALACGLLAVSLGSASLSAQEPQELVAEQQDSEINPQTEESQDPAPFL 61	FT	TRANSMEM	24	44	EXTRACELLULAR (POTENTIAL).
Qy	86	NRLVRPRSPAKGRKTARRATAAHYEVHPRPCQDGAAQGVDGTSGWEARINSSSPLR 145	FT	DOMAIN	45	272	CLEAVAGE (BY SIMILARITY).
Db	62	EDLVRPRSPAKGRKARPRRAAAYHEVHPRPCQDGAAQGVDGTGSWEETKINSSSPLR 121	FT	DISULFID SITE	110	111	POTENTIAL.
Qy	146	YNRQIGEFLIVTRAGLYLYCQVHFDLEGKAVYLKLDDLVNGYLALRCLEEFSAASSLGP 205	FT	CARBONYD	124	124	N-LINKED (GLCNAC, .) (POTENTIAL).
Db	122	YDRQIGEFTVIRAGLYLYCQVHFDLEGKAVYLKLDDLVNGYLALRCLEEFSAASSLGP 181	FT	CARBONYD	146	146	N-LINKED (GLCNAC, .) (POTENTIAL).
Db	182	QRLQCQVSGLLALRPGSSLRIRTLPWHLKARPLTFYFGLFQVH 249	FT	SEQUENCE	251	251	N-LINKED (GLCNAC, .) (POTENTIAL).
Qy	206	QRLQCQVSGLLALRPGSSLRIRTLPWHLKARPLTFYFGLFQVH 249	SQ	SEQUENCE	272	AA;	5409824A8E53CCD7 CRC64;
Db	182	QRLQCQVSGLLALRPGSSLRIRTLPWHLKARPLTFYFGLFQVH 225	Qy	Query Match	8	61;	Score 109.5;
FT	RESULT 3	Best Local Similarity	26.4%;	DB 1;	Best Local Similarity	26.4%;	Pred. No. 0.0377;
FT	TNFS5_CHICK	STANDARD;	Matches 42;	DB 1;	Matches 42;	26;	Indels 33; Gaps 7;
AC	Q918D8;	PRT;	272 AA.	Qy	104	RRAIAAHYEVHPRPGDGAQGVDTGTVSGW EARINSSSSPLRNYRQIGEFTVIRAGLYY 162	
DT	15-JUN-2002	(Rel. 41, Created)	Db	133	RQPIATHLA-----GVKNTTVRLKMTTSYAPTSLISVHE-----GRKVKEVAGLYY 182		
DT	15-JUN-2002	(Rel. 41, Last sequence update)	Qy	163	LYCQVEFDFEGA-----VYLKLDLVQDVLALRCLEESATASSLGPQLRQCQV----- 212		
DT	15-JUN-2002	(Rel. 41, Last annotation update)	Db	183	YSQVSPCTKZASASAPFTLYLYLPMEDRL--MKGLDTHSTSTA-----LGELQS 233		
DE	Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-L)	DE	Qy	213	--SGLLALRPGSSLRIRTLFWHLKAAPEFTYFGLFQV 248		
DE	(CD154 Protein)	DE	Db	234	TREGGGYFELRQGDMYEVNVTSTAVNVNPGRNTYFGMFKL 272		
GN	TNFS5 OR CD40LG	GN	RESULT 4	TPN5_CANFA	SEQUENCE FROM N.A.		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianinae; Gallus.	OC	ID	TPN5_CANFA	SEQUENCE FROM N.A.		
OC	NCBI_TaxID=9031;	OC	ID	TPN5_CANFA	SEQUENCE FROM N.A.		
RN	[1]	OX	AC	097626;	AC	097626;	
RP	SEQUENCE FROM N.A.	RP	DT	16-OCT-2001 (Rel. 40, Created)	DT	16-OCT-2001 (Rel. 40, Last sequence update)	
RC	STRAIN:White leghorn; TISSUE=Spleen;	RC	DT	16-OCT-2001 (Rel. 40, Last annotation update)	DT	15-JUN-2002 (Rel. 41, Last annotation update)	
RA	Tregaskies C.A., Young J.R., Burnside J.;	RA	DE	Tumor necrosis factor ligand superfamily member 5 (CD40 ligand).	DE	Tumor necrosis factor ligand superfamily member 5 (CD40 ligand).	
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.	RL	GN	TNFS5 OR CD40LG OR CD40LG	GN	TNFS5 OR CD40LG OR CD40LG	
CC	FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell proliferation in the absence of co-stimulus as well as IgE production in the presence of IL-4. Involved in immunoglobulin class switching (By similarity).	CC	OS	Canis familiaris (Dog).	OS	Canis familiaris (Dog).	
CC	-!- SUBUNIT: Homotrimer (By similarity).	CC	OC	Mammalia; Eutheria; Carnivora; Pissipedia; Canidae; Canis.	OC	Mammalia; Eutheria; Carnivora; Pissipedia; Canidae; Canis.	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	RN	[1]	RN	[1]	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	RA	RA	RA	RA	
CC	-!- SUBUNIT: HOMOTRIMER (By similarity).	CC	RT	"Adjuvant properties of canine CD40L."	RT	"Adjuvant properties of canine CD40L."	
CC	-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM (By similarity).	CC	RJ	Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.	RJ	Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.	
CC	-!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell proliferation in the absence of co-stimulus as well as IgE production in the presence of IL-4. Involved in immunoglobulin class switching (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PROTEOLYTIC PROCESSING (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC	CC	CC	CC	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).	CC	CC	CC	CC	CC	
CC	-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).	CC	CC	CC	CC	CC	
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	CC				

DR HSSP; P29965; ITALY.
 DR InterPro; IPR003263; TNF_5.
 DR InterPro; IPR003536; TNF_abc.
 DR InterPro; IPR00478; TNF_family.
 DR Pfam; PF00229; TNF; 1.
 DR ProDom; PDD08600; TNF_5; 1.
 DR SMART; SMART0207; TNF; 1.
 DR SMART; SMART0207; TNF; 1.
 DR PSORT; PS00251; TNF_1; 1.
 DR PROSITE; PS50049; TNF_2; 1.
 DR PROSITE; PS50049; TNF_2; 1.
 DR Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
 CHAIN 1 260 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 MEMBER 5, MEMBRANE FORM.
 MEMBER 5, SOLUBLE FORM (BY SIMILARITY).
 FT DOMAIN 1 22 CYTOPLASMIC (TYPE-II MEMBRANE PROTEIN).
 FT TRANSMEM 23 46 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT DOMAIN 47 260 (POTENTIAL).
 FT SITE 111 112 EXTRACELLULAR (POTENTIAL).
 FT DISULFID 177 217 CLEAVAGE (BY SIMILARITY).
 FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SEQUENCE 260 AA; 28688 MN; 604F69A19E98EB70 CRC64;
 Best Local Similarity 25.5%; Score 108.5; DB 1; Length 260;
 Matches 53; Conservative 23; Mismatches 69; Indels 63; Gaps 8;

Query Match Score 95.5; DB 1; Length 201;
 Best Local Similarity 23.2%; Pred. No. 0.39; Mismatches 27; Indels 35; Gaps 9;
 Matches 44; Conservation 1/27;

Qy 54 EPAQEELVAAE--DQDPS-ELNPCTEEESODPAPLNRLVRPPIRRAKTRARRATAAH 110
 Db 103 EMKREENTIAMOKGQDPRIAHTYSEASNPASL----RWAPKGYYTISSNLVSL- 154

Qy 111 YEVHPRPGDGAQGVGDGTWSGEARINSSSPRLRNQIGEFTVTRAGLXYLCQVHFD 170
 Db 155 -----ENKGQ-----LAVKRGGLYVYYAQTFCC 177

Qy 171 EGKAVYLKDLLVGVLAIRCLEPFSAT-----AASSLGQLRCQVS---GLLAIPR 220
 Db 178 SNRQASSQAPF----VASILCLHSPCTERVLLRAASSRGSSKPCGQSQSIHLGGVFLHP 232

Qy 221 GSSHIRLTPWAHHLKAAPPLTYFGLFQV 248
 Db 233 GASVFVNNTDPDSQVSHRGFTSFLKL 260

RESULT 5
 TNFB_MACEU STANDARD; PRT; 201 AA.
 AC Q9ATX48; 16-OCT-2001 (Rel. 40, Created)
 F 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lymphotoxin-alpha Precursor (LT-alpha) (TNF-beta) (Tumor necrosis factor ligand superfamily member 1).
 OS LTA OR TNFSF1 OR TNFB.
 OC Macropus eugenii (Tammar wallaby).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Diproctodonta; Macropodidae; Macropus.
 OC NCBI_TaxID=9315;
 RN [1] Homo Sapiens (Human).
 RP SEQUENCE FROM N.A. Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa. Standard; PRT; 254 AA.
 RX MEDLINE=94374434; PubMed=0088337;
 RA Alderson M.R., Smith C.A., Armitage R.J., Davis-Smith T., Davis-Smith R.W., Falk B., Roux E., Baker E., Sutherland G.R., Goodwin R.G.;
 RA "Molecular and biological characterization of human 4-1BB and its ligand.";
 RL Eur. J. Immunol. 24:2219-2227(1994).
 CC -!- FUNCTION: Cytokine that binds to TNFRSF1B/TNFB and TNFRSF14/HEM. In its heterotrimeric form with LTb binds to TNFRSF1B/TNFB. Lymphotoxin is produced by lymphocytes and cytotoxic for a wide range of tumor cells in vitro and in vivo.
 CC -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTb and one LTa subunits or (less prevalent) two LTa and one LTb subunits (By similarity).
 CC

RESULT 6
 TNF9_HUMAN STANDARD; PRT; 254 AA.
 AC P4173; 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 9 (4-1BB ligand) (4-1BB).
 DE DB1BLU.
 GN TNFSF9.
 OS Homo Sapiens (Human).
 OC Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE=94374434; PubMed=0088337;
 RX DNA Seq. 10:399-403(2000).
 CC -!- Cytokine that in its homotrimeric form binds to TNFRSF1A/TNFRSF1B/TNFB and TNFRSF14/HEM. In its heterotrimeric form with LTb binds to TNFRSF1B/TNFB. Lymphotoxin is produced by lymphocytes and cytotoxic for a wide range of tumor cells in vitro and in vivo.
 CC -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTb and one LTa subunits or (less prevalent) two LTa and one LTb subunits (By similarity).
 CC

SEQUENCE FROM N.A. (ISOFORM 1).
 MEDLINE=98122340; PubMed=5462508;
 RA Mauri D.N., Ebner R., Montgomery R.I., Kochel K.D., Cheung T.C., Spear P.G.,
 RA Yu G.-L., Ruben S., Murphy M., Eisenberg R.J., Cohen G.H.,
 RA Ware C.F.;
 RT "LIGHT, a new member of the TNF superfamily, and lymphotxin alpha are
 RT ligands for herpesvirus entry mediator.";
 RT Immunity 8:21-30(1998).
 RN [2]
 RN [2]
 SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
 TISSUE=Liver;
 MEDLINE=98030532; PubMed=9765287;
 RX Harrop J.A., McDonnell P.C., Brigham-Burke M., Lyn S.D., Minton J.,
 RA Tan K.B., Dede K., Spampinato J., Silverman C., Hensley P.,
 RA DiPrinzio R., Emery J.G., Deen K., Eichman C., Chabot-Fletcher M.,
 RA Truneh A., Young P.R.;
 RA "Herpesvirus entry mediator ligand (HVEM-L), a novel ligand for
 RT HVEM/TR2, stimulates proliferation of T cells and inhibits HT29 cell
 RT growth.,"
 RT J. Biol. Chem. 273:27548-27556(1998).
 RN [3]
 SEQUENCE FROM N.A. (ISOFORM 2), AND PROCESSING.
 TISSUE=Brain;
 MEDLINE=21528948; PubMed=1167323;
 RA Granger S.W., Butrovich K.D., Housmand P., Ware C.F.;
 RA "Genomic characterization of LIGHT reveals linkage to an immune
 RT response locus on chromosome 19p13.3 and distinct isoforms generated
 by alternative splicing or proteolysis.,"
 RT J. Immunol. 167:5122-5128(2001).
 RN [4]
 SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RP TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (PC)-2001) to the EMBL/GenBank/DDBJ databases;
 CC -|- FUNCTION: Cytokine that binds to TNFRSF3/LTBR. Binding to the
 CC decoy receptor TNFRSF1B modulates its effects. Activates NFkB,
 CC stimulates the proliferation of T cells, and inhibits growth of
 CC the adenocarcinoma HT-29. Acts as a receptor for Herpes simplex
 CC virus.
 CC -|- SUBUNIT: Homotrimer.
 CC -|- SUBCELLULAR LOCATION: Type I I membrane protein and secreted
 CC (isoform 1); Cysoplasmic (isoform 2).
 CC -|- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2/LIGHT
 CC -|- delta-TM; are produced by alternative splicing.
 CC -|- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE SPLEEN BUT ALSO
 CC FOUND IN THE BRAIN; WEAKLY EXPRESSED IN PERIPHERAL LYMPHOID
 CC TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND KIDNEY,
 CC AND NO EXPRESSION SEEN IN FETAL TISSUES, ENDOCRINE GLANDS, OR
 CC NONHEMATOPOIETIC TUMOR LINES.
 CC -|- INDUCTION: UPREGULATED AFTER T-CELL ACTIVATION.
 CC -|- PTM: N-glycosylated.
 CC -|- PTM: The soluble form of isoform 1 derives from the membrane
 CC form by proteolytic processing.
 CC -|- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -|- SIMILARITY: Ref.4 sequence differs from that shown due to a
 CC frameshift in position 178.
 CC
 DR This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: AF036581; AAC39563.1; -;
 DR EMBL: AF06190; AAC25169.1; -;
 DR EMBL: AY028261; AAC26160.1; -;
 DR EMBL: BC018058; AAB18058.1; ALT_FRAME.
 DR HSSP: P01375; 4TSV.
 DR Genew: HNCN:11930; TNFSF14.
 MIM: 604520;
 DR DR InterPro: IPR000336; TNF_abc.
 DR InterPro: IPR000478; TNF_abc.
 DR DR

PFam: PF00229; TNF; 1.	ProDom: PDO02012; TNF_abc; 1.	SMART: SM00207; TNF; 1.	PROSITE: PS00251; TNF; 1; FALSE_NEG.	Cytokine; Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Alternative splicing.
CHAIN 1 240	CHAIN 1 240	TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 14, MEMBRANE FORM.	TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 14, SOLUBLE FORM.	
CHAIN 1 783	CHAIN 1 240			
DOMAIN 1 37	DOMAIN 1 37	CYTOPLASMIC (POTENTIAL).	CYTOPLASMIC (POTENTIAL).	
TRANSMEM 38 58	TRANSMEM 38 58	SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN) (POTENTIAL).	SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN) (POTENTIAL).	
DOMAIN 1 59	DOMAIN 1 59	EXTRACELLULAR (POTENTIAL).	EXTRACELLULAR (POTENTIAL).	
SITE 82 83	SITE 82 83	CLEAVAGE (POTENTIAL).	CLEAVAGE (POTENTIAL).	
DISULFID 154 187	DISULFID 154 187	POTENTIAL.	POTENTIAL.	
CARBONID 102 102	CARBONID 102 102	N-LINKED (GLCNAC).	N-LINKED (GLCNAC).	
VARSPLIC 38 73	VARSPLIC 38 73	MISSING (IN ISOFORM 2).	MISSING (IN ISOFORM 2).	
CONFFLICT 120 120	CONFFLICT 120 120	L -> V (IN REF. 4).	L -> V (IN REF. 4).	
CONFFLICT 214 214	CONFFLICT 214 214	E -> K (IN REF. 2).	E -> K (IN REF. 2).	
SEQUENCE 240 AA; 26351 MW; 490DBF67E1390B39 CRC64;	SEQUENCE 240 AA; 26351 MW; 490DBF67E1390B39 CRC64;			
Query Match 7.2%; Score 91.5; DB 1; Length 240;	Query Match 7.2%; Score 91.5; DB 1; Length 240;			
Best Local Similarity 25.0%; Pred. No. 1; Mismatches 18; Gaps 7;	Best Local Similarity 25.0%; Pred. No. 1; Mismatches 18; Gaps 7;			
Matches 44; Conservative 44; Gaps 7; Indels 67; Gaps 7;	Matches 44; Conservative 44; Gaps 7; Indels 67; Gaps 7;			
5 RSGRRG-RRGEFGTALLVPLAIGLGLALAIGLILLAVSLSGASLQAQEPQEEVLAE 63	5 RSGRRG-RRGEFGTALLVPLAIGLGLALAIGLILLAVSLSGASLQAQEPQEEVLAE 63			
26 RSHRQSSVARVIGLIGL-LIIMQAGLAVQGVWELQLHLWRLG----ENV- 69	26 RSHRQSSVARVIGLIGL-LIIMQAGLAVQGVWELQLHLWRLG----ENV- 69			
64 EDQDPSLENPOTEEQSDQAPDPAPLNLVRPERSAPKGRKTRARRAIAAHYEVHPRGODGAQ 123	64 EDQDPSLENPOTEEQSDQAPDPAPLNLVRPERSAPKGRKTRARRAIAAHYEVHPRGODGAQ 123			
70 -----T-TRPDGPGASWKEIQLERS-----HEVNPAHHTGAN 102	70 -----T-TRPDGPGASWKEIQLERS-----HEVNPAHHTGAN 102			
124 AGYDGTGTVGWEARRNSSSPLRVRNQI-----GEFYVTRAGLGYLYQCV 167	124 AGYDGTGTVGWEARRNSSSPLRVRNQI-----GEFYVTRAGLGYLYQCV 167			
103 SSSLTG-----SCGPLLWETQQLGLAFRLRGSLSYHDGALVVTKGAGYYIVSKV 147	103 SSSLTG-----SCGPLLWETQQLGLAFRLRGSLSYHDGALVVTKGAGYYIVSKV 147			
CG22_ANIMA STANDARD; PRT; 441 AA.	CG22_ANIMA STANDARD; PRT; 441 AA.			
P348701; 01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence update)	P348701; 01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence update)			
16-OCT-2001 (Rel. 40, Last annotation update) G2/mitotic-specific cyclin 2 (Garden snapdragon).	16-OCT-2001 (Rel. 40, Last annotation update) G2/mitotic-specific cyclin 2 (Garden snapdragon).			
Antirrhinum majus (Garden snapdragon).	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eudicots; core eudicots; Asteridae; eudicots 1; Lamiaceae; Antirrhinum. [1]			
SEQUENCE FROM N.A. MEDLINE:94148008; PubMed=8311906; Robert P.R., Coen E.S., Murphy G.J.P., Doonan J.H.; "Patterns of cell division revealed by transcriptional regulation of genes during the cell cycle in plants."; EMBL J. 13:616-624 (1994).	SEQUENCE FROM N.A. MEDLINE:94148008; PubMed=8311906; Robert P.R., Coen E.S., Murphy G.J.P., Doonan J.H.; "Patterns of cell division revealed by transcriptional regulation of genes during the cell cycle in plants."; EMBL J. 13:616-624 (1994).			
-!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M (MITOSIS) TRANSITION. G2/M CYCLINS ACCUMULATE STEADILY DURING G2 AND ARE ABRUPTLY DESTROYED AT MITOSIS.	-!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M (MITOSIS) TRANSITION. G2/M CYCLINS ACCUMULATE STEADILY DURING G2 AND ARE ABRUPTLY DESTROYED AT MITOSIS.			
-!- SUBUNIT: INTERACTS WITH THE CDC2 AND CDK2 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE Holoenzyme COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.	-!- SUBUNIT: INTERACTS WITH THE CDC2 AND CDK2 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE Holoenzyme COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.			
-!- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS ABRUPTLY DESTROYED AT MITOSIS.	-!- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS ABRUPTLY DESTROYED AT MITOSIS.			
-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.	-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.			
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RESULTS 8	RESULTS 9			
CG22_ANIMA STANDARD; PRT; 441 AA.	JIP1_MOUSE STANDARD; PRT; 707 AA.			
P348701; 01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence update)	Q9WV79; Q9WV18; Q9WV17; Q9R1H9; Q9R1Z1; O35145; AC 15-JUN-2002 (Rel. 41, Last sequence update)			
16-OCT-2001 (Rel. 40, Last annotation update) G2/mitotic-specific cyclin 2 (Garden snapdragon).	DT 15-JUN-2002 (Rel. 41, Last annotation update) C-jun-amino-terminal-interacting protein 1 (JNK-interacting protein 1) (JNK1) (JNK MAP kinase scaffold protein 1) (Islet-brain-1) (IB-1) (Mitogen-activated protein kinase 8-interacting protein 1). DE			
Antirrhinum majus (Garden snapdragon).	DE MAPK1IP1 OR PRK8IP OR JIP1 OR IB1. OS Mus musculus (Mouse).			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eudicots; core eudicots; Asteridae; eudicots 1; Lamiaceae; Antirrhinum. [1]	OC Bokayota; Metzoo; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10030; RN SEQUENCE FROM N.A. (ISOFORM JIP-1A), AND POSSIBLE FUNCTION.			
CG22_ANIMA STANDARD; PRT; 441 AA.	JIP1_MOUSE STANDARD; PRT; 707 AA.			
P348701; 01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence update)	Q9WV79; Q9WV18; Q9WV17; Q9R1H9; Q9R1Z1; O35145; AC 15-JUN-2002 (Rel. 41, Last sequence update)			
16-OCT-2001 (Rel. 40, Last annotation update) G2/mitotic-specific cyclin 2 (Garden snapdragon).	DT 15-JUN-2002 (Rel. 41, Last sequence update) C-jun-amino-terminal-interacting protein 1 (JNK-interacting protein 1) (JNK1) (JNK MAP kinase scaffold protein 1) (Islet-brain-1) (IB-1) (Mitogen-activated protein kinase 8-interacting protein 1). DE			
Antirrhinum majus (Garden snapdragon).	DE MAPK1IP1 OR PRK8IP OR JIP1 OR IB1. OS Mus musculus (Mouse).			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eudicots; core eudicots; Asteridae; eudicots 1; Lamiaceae; Antirrhinum. [1]	OC Bokayota; Metzoo; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10030; RN SEQUENCE FROM N.A. (ISOFORM JIP-1A), AND POSSIBLE FUNCTION.			
CG22_ANIMA STANDARD; PRT; 441 AA.	JIP1_MOUSE STANDARD; PRT; 707 AA.			
P348701; 01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence update)	Q9WV79; Q9WV18; Q9WV17; Q9R1H9; Q9R1Z1; O35145; AC 15-JUN-2002 (Rel. 41, Last sequence update)			
16-OCT-2001 (Rel. 40, Last annotation update) G2/mitotic-specific cyclin 2 (Garden snapdragon).	DT 15-JUN-2002 (Rel. 41, Last sequence update) C-jun-amino-terminal-interacting protein 1 (JNK-interacting protein 1) (JNK1) (JNK MAP kinase scaffold protein 1) (Islet-brain-1) (IB-1) (Mitogen-activated protein kinase 8-interacting protein 1). DE			
Antirrhinum majus (Garden snapdragon).	DE MAPK1IP1 OR PRK8IP OR JIP1 OR IB1. OS Mus musculus (Mouse).			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eudicots; core eudicots; Asteridae; eudicots 1; Lamiaceae; Antirrhinum. [1]	OC Bokayota; Metzoo; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10030; RN SEQUENCE FROM N.A. (ISOFORM JIP-1A), AND POSSIBLE FUNCTION.			
CG22_ANIMA STANDARD; PRT; 441 AA.	JIP1_MOUSE STANDARD; PRT; 707 AA.			
P348701; 01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence update)	Q9WV79; Q9WV18; Q9WV17; Q9R1H9; Q9R1Z1; O35145; AC 15-JUN-2002 (Rel. 41, Last sequence update)			
16-OCT-2001 (Rel. 40, Last annotation update) G2/mitotic-specific cyclin 2 (Garden snapdragon).	DT 15-JUN-2002 (Rel. 41, Last sequence update) C-jun-amino-terminal-interacting protein 1 (JNK-interacting protein 1) (JNK1) (JNK MAP kinase scaffold protein 1) (Islet-brain-1) (IB-1) (Mitogen-activated protein kinase 8-interacting protein 1). DE			
Antirrhinum majus (Garden snapdragon).	DE MAPK1IP1 OR PRK8IP OR JIP1 OR IB1. OS Mus musculus (Mouse).			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eudicots; core eudicots; Asteridae; eudicots 1; Lamiaceae; Antirrhinum. [1]	OC Bokayota; Metzoo; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10030; RN SEQUENCE FROM N.A. (ISOFORM JIP-1A), AND POSSIBLE FUNCTION.			
CG22_ANIMA STANDARD; PRT; 441 AA.	JIP1_MOUSE STANDARD; PRT; 707 AA.			
P348701; 01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence update)	Q9WV79; Q9WV18; Q9WV17; Q9R1H9; Q9R1Z1; O35145; AC 15-JUN-2002 (Rel. 41, Last sequence update)			
16-OCT-2001 (Rel. 40, Last annotation update) G2/mitotic-specific cyclin 2 (Garden snapdragon).	DT 15-JUN-2002 (Rel. 41, Last sequence update) C-jun-amino-terminal-interacting protein 1 (JNK-interacting protein 1) (JNK1) (JNK MAP kinase scaffold protein 1) (Islet-brain-1) (IB-1) (Mitogen-activated protein kinase 8-interacting protein 1). DE			
Antirrhinum majus (Garden snapdragon).	DE MAPK1IP1 OR PRK8IP OR JIP1 OR IB1. OS Mus musculus (Mouse).			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eudicots; core eudicots; Asteridae; eudicots 1; Lamiaceae; Antirrhinum. [1]	OC Bokayota; Metzoo; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10030; RN SEQUENCE FROM N.A. (ISOFORM JIP-1A), AND POSSIBLE FUNCTION.			
CG22_ANIMA STANDARD; PRT; 441 AA.	JIP1_MOUSE STANDARD; PRT; 707 AA.			
P348701; 01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence update)	Q9WV79; Q9WV18; Q9WV17; Q9R1H9; Q9R1Z1; O35145; AC 15-JUN-2002 (Rel. 41, Last sequence update)			
16-OCT-2001 (Rel. 40, Last annotation update) G2/mitotic-specific cyclin 2 (Garden snapdragon).	DT 15-JUN-2002 (Rel. 41, Last sequence update) C-jun-amino-terminal-interacting protein 1 (JNK-interacting protein 1) (JNK1) (JNK MAP kinase scaffold protein 1) (Islet-brain-1) (IB-1) (Mitogen-activated protein kinase 8-interacting protein 1). DE			
Antirrhinum majus (Garden snapdragon).	DE MAPK1IP1 OR PRK8IP OR JIP1 OR IB1. OS Mus musculus (Mouse).			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eudicots; core eudicots; Asteridae; eudicots 1; Lamiaceae; Antirrhinum. [1]	OC Bokayota; Metzoo; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10030; RN SEQUENCE FROM N.A. (ISOFORM JIP-1A), AND POSSIBLE FUNCTION.			
CG22_ANIMA STANDARD; PRT; 441 AA.	JIP1_MOUSE STANDARD; PRT; 707 AA.			
P348701; 01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence update)	Q9WV79; Q9WV18; Q9WV17; Q9R1H9; Q9R1Z1; O35145; AC 15-JUN-2002 (Rel. 41, Last sequence update)			
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Antirrhinum majus (Garden snapdragon).	DE MAPK1IP1 OR PRK8IP OR JIP1 OR IB1. OS Mus musculus (Mouse).			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eudicots; core eudicots; Asteridae; eudicots 1; Lamiaceae; Antirrhinum. [1]	OC Bokayota; Metzoo; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10030; RN SEQUENCE FROM N.A. (ISOFORM JIP-1A), AND POSSIBLE FUNCTION.			
CG22_ANIMA STANDARD; PRT; 441 AA.	JIP1_MOUSE STANDARD; PRT; 707 AA.			
P348701; 01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence update)	Q9WV79; Q9WV18; Q9WV17; Q9R1H9; Q9R1Z1; O35145; AC 15-JUN-2002 (Rel. 41, Last sequence update)			
16-OCT-2001 (Rel. 40, Last annotation update) G2/mitotic-specific cyclin 2 (Garden snapdragon).	DT 15-JUN-2002 (Rel. 41, Last sequence update) C-jun-amino-terminal-interacting protein 1 (JNK-interacting protein 1) (JNK1) (JNK MAP kinase scaffold protein 1) (Islet-brain-1) (IB-1) (Mitogen-activated protein kinase 8-interacting protein 1). DE			
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eudicots; core eudicots; Asteridae; eudicots 1; Lamiaceae; Antirrhinum. [1]	OC Bokayota; Metzoo; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10030; RN SEQUENCE FROM N.A. (ISOFORM JIP-1A), AND POSSIBLE FUNCTION.			
CG22_ANIMA STANDARD; PRT; 441 AA.	JIP1_MOUSE STANDARD; PRT; 707 AA.			
P348701; 01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence update)	Q9WV79; Q9WV18; Q9WV17; Q9R1H9; Q9R1Z1; O35145; AC 15-JUN-2002 (Rel. 41, Last sequence update)			
16-OCT-2001 (Rel. 40, Last annotation update) G2/mitotic-specific cyclin 2 (Garden snapdragon).	DT 15-JUN-2002 (Rel. 41, Last sequence update) C-jun-amino-terminal-interacting protein 1 (JNK-interacting protein 1) (JNK1) (JNK MAP kinase scaffold protein 1) (Islet-brain-1) (IB-1) (Mitogen-activated protein kinase 8-interacting protein 1). DE			
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eudicots; core eudicots; Asteridae; eudicots 1; Lamiaceae; Antirrhinum. [1]	OC Bokayota; Metzoo; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10030; RN SEQUENCE FROM N.A. (ISOFORM JIP-1A), AND POSSIBLE FUNCTION.			
CG22_ANIMA STANDARD; PRT; 441 AA.	JIP1_MOUSE STANDARD; PRT; 707 AA.			
P348701; 01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence update)	Q9WV79; Q9WV18; Q9WV17; Q9R1H9; Q9R1Z1; O35145; AC 15-JUN-2002 (Rel. 41, Last sequence update)			
16-OCT-2001 (Rel. 40, Last annotation update) G2/mitotic-specific cyclin 2 (Garden snapdragon).	DT 15-JUN-2002 (Rel. 41, Last sequence update) C-jun-amino-terminal-interacting protein 1 (JNK-interacting protein 1) (JNK1) (JNK MAP kinase scaffold protein 1) (Islet-brain-1) (IB-1) (Mitogen-activated protein kinase 8-interacting protein 1). DE			
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eudicots; core eudicots; Asteridae; eudicots 1; Lamiaceae; Antirrhinum. [1]	OC Bokayota; Metzoo; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10030; RN SEQUENCE FROM N.A. (ISOFORM JIP-1A), AND POSSIBLE FUNCTION.			
CG22_ANIMA STANDARD; PRT; 441 AA.	JIP1_MOUSE STANDARD; PRT; 707 AA.			
P348701; 01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence update)	Q9WV79; Q9WV18; Q9WV17; Q9R1H9; Q9R1Z1; O35145; AC 15-JUN-2002 (Rel. 41, Last sequence update)			
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eudicots; core eudicots; Asteridae; eudicots 1; Lamiaceae; Antirrhinum. [1]	OC Bokayota; Metzoo; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10030; RN SEQUENCE FROM N.A. (ISOFORM JIP-1A), AND POSSIBLE FUNCTION.			
CG22_ANIMA STANDARD; PRT; 441 AA.	JIP1_MOUSE STANDARD; PRT; 707 AA.			
P348701; 01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence update)	Q9WV79; Q9WV18; Q9WV17; Q9R1H9; Q9R1Z1; O35145; AC 15-JUN-2002 (Rel. 41, Last sequence update)			
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eudicots; core eudicots; Asteridae; eudicots 1; Lamiaceae; Antirrhinum. [1]	OC Bokayota; Metzoo; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10030; RN SEQUENCE FROM N.A. (ISOFORM JIP-1A), AND POSSIBLE FUNCTION.			
CG22_ANIMA STANDARD; PRT; 441 AA.	JIP1_MOUSE STANDARD; PRT; 707 AA.			
P348701; 01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence update)	Q9WV79; Q9WV18; Q9WV17; Q9R1H9; Q9R1Z1; O35145; AC 15-JUN-2002 (Rel. 41, Last sequence update)			
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eudicots; core eudicots; Asteridae; eudicots 1; Lamiaceae; Antirrhinum. [1]	OC Bokayota; Metzoo; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10030; RN SEQUENCE FROM N.A. (ISOFORM JIP-1A), AND POSSIBLE FUNCTION.			
CG22_ANIMA STANDARD; PRT; 441 AA.	JIP1_MOUSE STANDARD; PRT; 707 AA.			
P348701; 01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence update)	Q9WV79; Q9WV18; Q9WV17; Q9R1H9; Q9R1Z1; O35145; AC 15-JUN-2002 (Rel. 41, Last sequence update)			
16-OCT-2001 (Rel. 40, Last annotation update) G2/mitotic-specific cyclin 2 (Garden snapdragon).	DT 15-JUN-2002 (Rel. 41, Last sequence update) C-jun-amino-terminal-interacting protein 1 (JNK-interacting protein 1) (JNK1) (JNK MAP kinase scaffold protein 1) (Islet-brain-1) (IB-1) (Mitogen-activated protein kinase 8-interacting protein 1). DE			
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eudicots; core eudicots; Asteridae; eudicots 1; Lamiaceae; Antirrhinum. [1]	OC Bokayota; Metzoo; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10030; RN SEQUENCE FROM N.A. (ISOFORM JIP-1A), AND POSSIBLE FUNCTION.			
CG22_ANIMA STANDARD; PRT; 441 AA.	JIP1_MOUSE STANDARD; PRT; 707 AA.			
P348701; 01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence update)	Q9WV79; Q9WV18; Q9WV17; Q9R1H9; Q9R1Z1; O35145; AC 15-JUN-2002 (Rel. 41, Last sequence update)			
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Antirrhinum majus (Garden snapdragon).	DE MAPK1IP1 OR PRK8IP OR JIP1 OR IB1. OS Mus musculus (Mouse).			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eudicots; core eudicots; Asteridae; eudicots 1; Lamiaceae; Antirrhinum. [1]	OC Bokayota; Metzoo; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10030; RN SEQUENCE FROM N.A. (ISOFORM JIP-1A), AND POSSIBLE FUNCTION.			
CG22_ANIMA STANDARD; PRT; 441 AA.	JIP1_MOUSE STANDARD; PRT; 707 AA.			
P348701; 01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence update)	Q9WV79; Q9WV18; Q9WV17; Q9R1H9; Q9R1Z1; O35145; AC 15-JUN-2002 (Rel. 41, Last sequence update)			
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Antirrhinum majus (Garden snapdragon).	DE MAPK1IP1 OR PRK8IP OR JIP1 OR IB1. OS Mus musculus (Mouse).</			

FT	CARBHYD	95	95	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	204 AA;	22098 MW;	E249F0A2CEDBS425 CRC64;
Query Match		6.9%;	Score 87;	DB 1; Length 204;
Best Local Matches	58;	Conservative	29;	Mismatches 89; Indels 78; Gaps 13;
Qy	16	PGTALLY----PLALGLGLALLACIGLILAVVSLGSRA---SLSAQEPQQEELVAAEEDQD 67		
Db	4	PGRLYLLRVCSTPPLLGLLAA----LPLAEQGLRGIGLTLPSAAQPAHQL----- 51		
Qy	68	PSELPQTEESQDPAFLNLVRPERSAKPGRTRARRAIAAHVEHPPGQDQAQAGYD 127		
Db	52	-----PPIPFTGTLKP-----AHLVGDST-QSLR----- 77		
Qy	128	GTWSGWEARINSSSP-DRYNQOI---GEFIVTURAGLYLYCQVHFDEGRA-----V 175		
Db	78	-----W-----RANTDRAFTLHGFSLSNNSLVLPSPGLIFTYPSQVTF-SGRGCFPRATPPL 128		
Qy	176	YLKLUDLLV---DGYLALRCLEESATAASSLGQPLQURLCQVSGJLALRPGSSLRIRTLPWA 232		
Db	129	YLAHQLVQLFSPQYPHPVPLLSAQKSVCVSPGQPMWRSVYQQGAVFLTRQDLSHTDGTG 188		
Qy	233	HIIKAPFLTYFGLF 246		
Db	189	HLLSPSPSYFFGAF 202		
RESULT 12				
FT	TN10_MOUSE	ID	STANDARD;	PRT; 291 AA.
SQ	P50592;	01-OCT-1996	(Rel. 34, Created)	
RA	01-OCT-1996	(Rel. 34, Last sequence update)		
RA	15-JUN-2002	(Rel. 41, Last annotation update)		
DE	Tumor necrosis factor ligand superfamily member 10 (TNF-related apoptosis inducing ligand) (TRAIL protein).			
GN	TNFSF10 OR TRAIL.			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=100990; [1]			
RN	SEQUENCE FROM N.A. MEDLINE-96111955; PubMed=8777713; Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P., Goodwin J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A., Goodwin P.G.; "Identification and characterization of a new member of the TNF family that induces apoptosis."; Immunity 3:673-682 (1995).			
RA	-!- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1, TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and possibly also to TNFRSF11B/ORG. Induces apoptosis. Its activity may be modulated by binding to the decoy receptors TNFRSF10/TRAIR3, TNFRSF10D/TRAIR4 and TNFRSF11B/ORG that cannot induce apoptosis.			
CC	-!- SUBUNIT: HOMOTRIMER (By similarity).			
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).			
CC	-!- TISSUE SPECIFICITY: WIDESCREEN.			
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.			
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CC	EMBL; MGDB; PDB; HSSP; PSSM; IDOG; Tmfss10;			
CC	DR	InterPro; IPR003636; TNF abc.		
CC	DR	InterPro; IPR000418; TNF_-family.		
CC	DR	Pfam; PF00223; TNF; 1.		
CC	DR	ProDom; PD000012; TNF abc; 1.		
CC	DR	SMART; SM00207; TNF; 1.		
CC	DR	PROSITE; PS00251; TNF; 2; 1.		
CC	KW	Cytokine; Transmembrane; Signal-anchor: Apoptosis.		
CC	FT	DOMAIN 1 17 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)		
CC	FT	TRANSMEM 18 38 (POTENTIAL).		
CC	FT	DOMAIN 39 291 EXTRACELLULAR (POTENTIAL).		
CC	FT	CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).		
CC	SQ	SEQUENCE 291 AA; 3347 MN; 3FEACB9F0D7B02 CRC64;		
RESULT 13				
FT	Y1497_MYCTU	ID	STANDARD;	PRT; 310 AA.
SQ	58	ELVVAEEDQDPSELNPQTEESQDPAPFLNRLVPRRSPAP--KGRKTRARRATAAHAYEVH 115		
Db	93	EEVTLRQTDTISTVPEQLSPPLP--RGGRQPKVAAHTGTRITRSNSALIP----- 143		
Qy	116	RPGDGAAQAGVQDVTSGEAEARINSSSPFLRINRQIGEFLVTRAGLYLYCQVHF 169		
Db	144	-1SKDGKTLG--QKIESWESSRKGHSTFLNHVLFRNGELVIEQEGLYVYSSQTYF 194		
RESULT 14				
FT	Y1497_MYCTU	ID	STANDARD;	PRT; 310 AA.
SQ	58	ELVVAEEDQDPSELNPQTEESQDPAPFLNRLVPRRSPAP--KGRKTRARRATAAHAYEVH 115		
Db	93	EEVTLRQTDTISTVPEQLSPPLP--RGGRQPKVAAHTGTRITRSNSALIP----- 143		
Qy	116	RPGDGAAQAGVQDVTSGEAEARINSSSPFLRINRQIGEFLVTRAGLYLYCQVHF 169		
Db	144	-1SKDGKTLG--QKIESWESSRKGHSTFLNHVLFRNGELVIEQEGLYVYSSQTYF 194		
RESULT 15				
FT	Y1497_MYCTU	ID	STANDARD;	PRT; 310 AA.
SQ	58	ELVVAEEDQDPSELNPQTEESQDPAPFLNRLVPRRSPAP--KGRKTRARRATAAHAYEVH 115		
Db	93	EEVTLRQTDTISTVPEQLSPPLP--RGGRQPKVAAHTGTRITRSNSALIP----- 143		
Qy	116	RPGDGAAQAGVQDVTSGEAEARINSSSPFLRINRQIGEFLVTRAGLYLYCQVHF 169		
Db	144	-1SKDGKTLG--QKIESWESSRKGHSTFLNHVLFRNGELVIEQEGLYVYSSQTYF 194		
RESULT 16				
FT	Y1497_MYCTU	ID	STANDARD;	PRT; 310 AA.
SQ	58	ELVVAEEDQDPSELNPQTEESQDPAPFLNRLVPRRSPAP--KGRKTRARRATAAHAYEVH 115		
Db	93	EEVTLRQTDTISTVPEQLSPPLP--RGGRQPKVAAHTGTRITRSNSALIP----- 143		
Qy	116	RPGDGAAQAGVQDVTSGEAEARINSSSPFLRINRQIGEFLVTRAGLYLYCQVHF 169		
Db	144	-1SKDGKTLG--QKIESWESSRKGHSTFLNHVLFRNGELVIEQEGLYVYSSQTYF 194		
RESULT 17				
FT	Y1497_MYCTU	ID	STANDARD;	PRT; 310 AA.
SQ	58	ELVVAEEDQDPSELNPQTEESQDPAPFLNRLVPRRSPAP--KGRKTRARRATAAHAYEVH 115		
Db	93	EEVTLRQTDTISTVPEQLSPPLP--RGGRQPKVAAHTGTRITRSNSALIP----- 143		
Qy	116	RPGDGAAQAGVQDVTSGEAEARINSSSPFLRINRQIGEFLVTRAGLYLYCQVHF 169		
Db	144	-1SKDGKTLG--QKIESWESSRKGHSTFLNHVLFRNGELVIEQEGLYVYSSQTYF 194		
RESULT 18				
FT	Y1497_MYCTU	ID	STANDARD;	PRT; 310 AA.
SQ	58	ELVVAEEDQDPSELNPQTEESQDPAPFLNRLVPRRSPAP--KGRKTRARRATAAHAYEVH 115		
Db	93	EEVTLRQTDTISTVPEQLSPPLP--RGGRQPKVAAHTGTRITRSNSALIP----- 143		
Qy	116	RPGDGAAQAGVQDVTSGEAEARINSSSPFLRINRQIGEFLVTRAGLYLYCQVHF 169		
Db	144	-1SKDGKTLG--QKIESWESSRKGHSTFLNHVLFRNGELVIEQEGLYVYSSQTYF 194		
RESULT 19				
FT	Y1497_MYCTU	ID	STANDARD;	PRT; 310 AA.
SQ	58	ELVVAEEDQDPSELNPQTEESQDPAPFLNRLVPRRSPAP--KGRKTRARRATAAHAYEVH 115		
Db	93	EEVTLRQTDTISTVPEQLSPPLP--RGGRQPKVAAHTGTRITRSNSALIP----- 143		
Qy	116	RPGDGAAQAGVQDVTSGEAEARINSSSPFLRINRQIGEFLVTRAGLYLYCQVHF 169		
Db	144	-1SKDGKTLG--QKIESWESSRKGHSTFLNHVLFRNGELVIEQEGLYVYSSQTYF 194		
RESULT 20				
FT	Y1497_MYCTU	ID	STANDARD;	PRT; 310 AA.
SQ	58	ELVVAEEDQDPSELNPQTEESQDPAPFLNRLVPRRSPAP--KGRKTRARRATAAHAYEVH 115		
Db	93	EEVTLRQTDTISTVPEQLSPPLP--RGGRQPKVAAHTGTRITRSNSALIP----- 143		
Qy	116	RPGDGAAQAGVQDVTSGEAEARINSSSPFLRINRQIGEFLVTRAGLYLYCQVHF 169		
Db	144	-1SKDGKTLG--QKIESWESSRKGHSTFLNHVLFRNGELVIEQEGLYVYSSQTYF 194		
RESULT 21				
FT	Y1497_MYCTU	ID	STANDARD;	PRT; 310 AA.
SQ	58	ELVVAEEDQDPSELNPQTEESQDPAPFLNRLVPRRSPAP--KGRKTRARRATAAHAYEVH 115		
Db	93	EEVTLRQTDTISTVPEQLSPPLP--RGGRQPKVAAHTGTRITRSNSALIP----- 143		
Qy	116	RPGDGAAQAGVQDVTSGEAEARINSSSPFLRINRQIGEFLVTRAGLYLYCQVHF 169		
Db	144	-1SKDGKTLG--QKIESWESSRKGHSTFLNHVLFRNGELVIEQEGLYVYSSQTYF 194		
RESULT 22				
FT	Y1497_MYCTU	ID	STANDARD;	PRT; 310 AA.
SQ	58	ELVVAEEDQDPSELNPQTEESQDPAPFLNRLVPRRSPAP--KGRKTRARRATAAHAYEVH 115		
Db	93	EEVTLRQTDTISTVPEQLSPPLP--RGGRQPKVAAHTGTRITRSNSALIP----- 143		
Qy	116	RPGDGAAQAGVQDVTSGEAEARINSSSPFLRINRQIGEFLVTRAGLYLYCQVHF 169		
Db	144	-1SKDGKTLG--QKIESWESSRKGHSTFLNHVLFRNGELVIEQEGLYVYSSQTYF 194		
RESULT 23				
FT	Y1497_MYCTU	ID	STANDARD;	PRT; 310 AA.
SQ	58	ELVVAEEDQDPSELNPQTEESQDPAPFLNRLVPRRSPAP--KGRKTRARRATAAHAYEVH 115		
Db	93	EEVTLRQTDTISTVPEQLSPPLP--RGGRQPKVAAHTGTRITRSNSALIP----- 143		
Qy	116	RPGDGAAQAGVQDVTSGEAEARINSSSPFLRINRQIGEFLVTRAGLYLYCQVHF 169		
Db	144	-1SKDGKTLG--QKIESWESSRKGHSTFLNHVLFRNGELVIEQEGLYVYSSQTYF 194		
RESULT 24				
FT	Y1497_MYCTU	ID	STANDARD;	PRT; 310 AA.
SQ	58	ELVVAEEDQDPSELNPQTEESQDPAPFLNRLVPRRSPAP--KGRKTRARRATAAHAYEVH 115		
Db	93	EEVTLRQTDTISTVPEQLSPPLP--RGGRQPKVAAHTGTRITRSNSALIP----- 143		
Qy	116	RPGDGAAQAGVQDVTSGEAEARINSSSPFLRINRQIGEFLVTRAGLYLYCQVHF 169		
Db	144	-1SKDGKTLG--QKIESWESSRKGHSTFLNHVLFRNGELVIEQEGLYVYSSQTYF 194		
RESULT 25				
FT	Y1497_MYCTU	ID	STANDARD;	PRT; 310 AA.
SQ	58	ELVVAEEDQDPSELNPQTEESQDPAPFLNRLVPRRSPAP--KGRKTRARRATAAHAYEVH 115		
Db	93	EEVTLRQTDTISTVPEQLSPPLP--RGGRQPKVAAHTGTRITRSNSALIP----- 143		
Qy	116	RPGDGAAQAGVQDVTSGEAEARINSSSPFLRINRQIGEFLVTRAGLYLYCQVHF 169		
Db	144	-1SKDGKTLG--QKIESWESSRKGHSTFLNHVLFRNGELVIEQEGLYVYSSQTYF 194		
RESULT 26				
FT	Y1497_MYCTU	ID	STANDARD;	PRT; 310 AA.
SQ	58	ELVVAEEDQDPSELNPQTEESQDPAPFLNRLVPRRSPAP--KGRKTRARRATAAHAYEVH 115		
Db	93	EEVTLRQTDTISTVPEQLSPPLP--RGGRQPKVAAHTGTRITRSNSALIP----- 143		
Qy	116	RPGDGAAQAGVQDVTSGEAEARINSSSPFLRINRQIGEFLVTRAGLYLYCQVHF 169		
Db	144	-1SKDGKTLG--QKIESWESSRKGHSTFLNHVLFRNGELVIEQEGLYVYSSQTYF 194		
RESULT 27				
FT	Y1497_MYCTU	ID	STANDARD;	PRT; 310 AA.
SQ	58	ELVVAEEDQDPSELNPQTEESQDPAPFLNRLVPRRSPAP--KGRKTRARRATAAHAYEVH 115		
Db	93	EEVTLRQTDTISTVPEQLSPPLP--RGGRQPKVAAHTGTRITRSNSALIP----- 143		
Qy	116	RPGDGAAQAGVQDVTSGEAEARINSSSPFLRINRQIGEFLVTRAGLYLYCQVHF 169		
Db	144	-1SKDGKTLG--QKIESWESSRKGHSTFLNHVLFRNGELVIEQEGLYVYSSQTYF 194		
RESULT 28				
FT	Y1497_MYCTU	ID	STANDARD;	PRT; 310 AA.
SQ	58	ELVVAEEDQDPSELNPQTEESQDPAPFLNRLVPRRSPAP--KGRKTRARRATAAHAYEVH 115		
Db	93	EEVTLRQTDTISTVPEQLSPPLP--RGGRQPKVAAHTGTRITRSNSALIP----- 143		
Qy	116	RPGDGAAQAGVQDVTSGEAEARINSSSPFLRINRQIGEFLVTRAGLYLYCQVHF 169		
Db	144	-1SKDGKTLG--QKIESWESSRKGHSTFLNHVLFRNGELVIEQEGLYVYSSQTYF 194		
RESULT 29				
FT	Y1497_MYCTU	ID	STANDARD;	PRT; 310 AA.
SQ	58	ELVVAEEDQDPSELNPQTEESQDPAPFLNRLVPRRSPAP--KGRKTRARRATAAHAYEVH 115		
Db	93	EEVTLRQTDTISTVPEQLSPPLP--RGGRQPKVAAHTGTRITRSNSALIP----- 143		
Qy	116	RPGDGAAQAGVQDVTSGEAEARINSSSPFLRINRQIGEFLVTRAGLYLYCQVHF 169		
Db	144	-1SKDGKTLG--QKIESWESSRKGHSTFLNHVLFRNGELVIEQEGLYVYSSQTYF 194		
RESULT 30				
FT	Y1497_MYCTU	ID	STANDARD;	PRT; 310 AA.
SQ	58	ELVVAEEDQDPSELNPQTEESQDPAPFLNRLVPRRSPAP--KGRKTRARRATAAHAYEVH 115		
Db	93	EEVTLRQTDTISTVPEQLSPPLP--RGGRQPKVAAHTGTRITRSNSALIP----- 143		
Qy	116	RPGDGAAQAGVQDVTSGEAEARINSSSPFLRINRQIGEFLVTRAGLYLYCQVHF 169		
Db	144	-1SKDGKTLG--QKIESWESSRKGHSTFLNHVLFRNGELVIEQEGLYVYSSQTYF 194		
RESULT 31				
FT	Y1497_MYCTU	ID	STANDARD;	PRT; 310 AA.
SQ	58	ELVVAEEDQDPSELNPQTEESQDPAPFLNRLVPRRSPAP--KGRKTRARRATAAHAYEVH 115		
Db	93	EEVTLRQTDTISTVPEQLSPPLP--RGGRQPKVAAHTGTRITRSNSALIP----- 143		
Qy	116	RPGDGAAQAGVQDVTSGEAEARINSSSPFLRINRQIGEFLVTRAGLYLYCQVHF 169		
Db	144	-1SKDGKTLG--QKIESWESSRKGHSTFLNHVLFRNGELVIEQEGLYVYSSQTYF 194		
RESULT 32				
FT	Y1497_MYCTU	ID	STANDARD;	PRT; 310 AA.
SQ	58	ELVVAEEDQDPSELNPQTEESQDPAPFLNRLVPRRSPAP--KGRKTRARRATAAHAYEVH 115		
Db	93	EEVTLRQTDTISTVPEQLSPPLP--RGGRQPKVAAHTGTRITRSNSALIP----- 143		
Qy	116	RPGDGAAQAGVQDVTSGEAEARINSSSPFLRINRQIGEFLVTRAGLYLYCQVHF 169		
Db	144	-1SKDGKTLG--QKIESWESSRKGHSTFLNHVLFRNGELVIEQEGLYVYSSQTYF 194		
RESULT 33				
FT	Y1497_MYCTU	ID	STANDARD;	PRT; 310 AA.
SQ	58	ELVVAEEDQDPSELNPQTEESQDPAPFLNRLVPRRSPAP--KGRKTRARRATAAHAYEVH 115		
Db	93	EEVTLRQTDTISTVPEQLSPPLP--RGGRQPKVAAHTGTRITRSNSALIP----- 143		
Qy	116	RPGDGAAQAGVQDVTSGEAEARINSSSPFLRINRQIGEFLVTRAGLYLYCQVHF 169		
Db	144	-1SKDGKTLG--QKIESWESSRKGHSTFLNHVLFRNGELVIEQEGLYVYSSQTYF 194		
RESULT 34				
FT	Y1497_MYCTU	ID	STANDARD;	PRT; 310 AA.
SQ	58	ELVVAEEDQDPSELNPQTEESQDPAPFLNRLVPRRSPAP--KGRKTRARRATAAHAYEVH 115		
Db	93	EEVTLRQTDTISTVPEQLSPPLP--RGGRQPKVAAHTGTRITRSNSALIP----- 143		
Qy	116	RPGDGAAQAGVQDVTSGEAEARINSSSPFLRINRQIGEFLVTRAGLYLYCQVHF 169		
Db	144	-1SKDGKTLG--QKIESWESSRKGHSTFLNHVLFRNGELVIEQEGLYVYSSQTYF 194		
RESULT 35				
FT	Y1497_MYCTU	ID	STANDARD;	PRT; 310 AA.
SQ	58	ELVVAEEDQDPSELNPQTEESQDPAPFLNRLVPRRSPAP--KGRKTRARRATAAHAYEVH 115		
Db	93	EEVTLRQTDTISTVPEQLSPPLP--RGGRQPKVAAHTGTRITRSNSALIP----- 143		
Qy	116	RPGDGAAQAGVQDVTSGEAEARINSSSPFLRINRQIGEFLVTRAGLYLYCQVHF 169		
Db	144	-1SKDGKTLG--QKIESWESSRKGHSTFLNHVLFRNGELVIEQEGLYVYSSQTYF 194		
RESULT 36				
FT	Y1497_MYCTU	ID	STANDARD;	PRT; 310 AA.
SQ	58	ELVVAEEDQDPSELNPQTEESQDPAPFLNRLVPRRSPAP--KGRKTRARRATAAHAYEVH 115		
Db	93	EEVTLRQTDTISTVPEQLSPPLP--RGGRQPKVAAHTGTRITRSNSALIP----- 143		
Qy	116	RPGDGAAQAGVQDVTSGEAEARINSSSPFLRINRQIGEFLVTRAGLYLYCQVHF 169		
Db	144	-1SKDGKTLG--QKIESWESSRKGHSTFLNHVLFRNGELVIEQEGLYVYSSQTYF 194		
RESULT 37				
FT	Y1497_MYCTU	ID	STANDARD;	PRT; 310 AA.
SQ	58	ELVVAEEDQDPSELNPQTEESQDPAPFLNRLVPRRSPAP--KGRKTRARRATAAHAYEVH 115		
Db	93	EEVTLRQTDTISTVPEQLSPPLP--RGGRQPKVAAHTGTRITRSNSALIP----- 143		
Qy	116	RPGDGAAQAGVQDVTSGEAEARINSSSPFLRINRQIGEFLVTRAGLYLYCQVHF 169		
Db	144	-1SKDGKTLG--QKIESWESSRKGHSTFLNHVLFRNGELVIEQEGLYVYSSQTYF 194		
RESULT 38				
FT	Y1497_MYCTU	ID	STANDARD;	PRT; 310 AA.
SQ	58	ELVVAEEDQDPSELNPQTEESQDPAPFLNRLVPRRSPAP--KGRKTRARRATAAHAYEVH 115		
Db	93	EEVTLRQTDTISTVPEQLSPPLP--RGGRQPKVAAHTGTRITRSNSALIP----- 143		
Qy	116	RPGDGAAQAGVQDVTSGEAEARINSSSPFLRINRQIGEFLVTRAGLYLYCQVHF 169		
Db	144	-1SKDGKTLG--QKIESWESSRKGHSTFLNHVLFRNGELVIEQEGLYVYSSQTYF 194		
RESULT 39				

GenCore version 5.1.4_p5-4578
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OM protein - protein search, using sw model

Run on: April 12, 2003, 08:38:15 ; Search time 32 Seconds

(without alignments)
1603.304 Million cell updates/sec

Title: US-09-905-810-2

Perfect score: 1268

Sequence: 1 MAARRSQRGRGRRGEGTAL..... PWAHLKAAPEFLTYFGFLFQVH 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Archived: 671580 seqs, 206047115 residues

Journal number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTRNMBL_21:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rrodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteria:*

17: sp_archeap:*

17	87	6.9	267	2
18	87	6.9	273	2
19	87	6.9	273	2
20	87	6.9	427	10
21	87	6.9	445	12
22	87	6.9	565	13
23	86.5	6.8	225	13
24	86.5	6.8	308	4
25	86.5	6.8	331	10
26	86.5	6.8	536	4
27	86.5	6.8	755	16
28	86.5	6.8	810	13
29	86	6.8	287	13
30	96	6.8	614	4
31	86	6.8	855	4
32	86	6.8	878	4
33	86	6.8	1294	5
34	86	6.8	1837	5
35	85.5	6.7	361	4
36	85.5	6.7	412	4
37	85	6.7	61374	1
38	85	6.7	431	10
39	84.5	6.7	402	2
40	84.5	6.7	450	16
41	84.5	6.7	748	5
42	84.5	6.7	9376	2
43	84	6.6	260	10
44	84	6.6	274	2
45	84	6.6	532	4
			Q96AP3	

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	325 AA.
ID	Q9V5G2			
AC	Q9V5G2;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	CG12919 protein.			
GN	CG12919.			
OS	Drosophila melanogaster (Fruit fly)			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriodea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7277;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BERKELEY;			
RX	MEDLINE=20196005; PubMed=10731132;			
RA	Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Amanatides P.G., Scheer S.E., Li P.W., Horskins R.A., Gallo R.P.,			
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
RA	Wootman J.R., Yandell M.D., Zhang Q., Chen L.X.,			
RA	Brandon R.C., Rogers Y.-H.C., Blaize R.G., Champé M., Peiffer B.D.,			
RA	Brandon D.A., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.C.,			
RA	Abrial J.F., Aghayani A., An H.-J., Andrews P.-F., Pfannkoch C., Baldwin D.,			
RA	Ballew R.M., Baxendale J., Bayraktaroglu L., Besly E.M.,			
RA	Beeson Y., Benos P.V., Berman B.P., Bhandari D., Bortsakov S.,			
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,			
RA	Burtis K.D., Butler H., Cadieu E., Center A., Chandra I.,			
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,			
RA	de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,			
RA	Dodson K.J., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunlap P.,			
RA	Durbin R.J., Evangelista C.C., Ferreria S., Fleischmann W.,			
RA	Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,			
RA	Glodner A., Gorre P., Gorre J.H., Harris M.,			
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,			
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,			
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Ketchum K.A.,			
RA	Kimmel B.E., Kodira C.D., Kraft C.D., Kravitz S., Lai Z.,			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query ID	Score	Match	Length	DB ID	Description
1	116	9.1	325	5	Q9V5G2	Q9v5g2 drosophila
2	95	7.6	643	16	Q9K217	Q9k217 streptomyce
3	94	7.5	375	16	Q9RH5	Q9rh5 deinococcus
4	94	7.4	937	16	Q93d1	Q93d1 streptomyce
5	93.5	7.4	776	16	Q9Rj01	Q9rj01 streptomyce
6	93	7.3	378	16	Q9AB9	Q9ab9 caulobacter
7	92.5	7.3	707	11	Q92J8	Q92j8 mus musculus
8	92	7.3	977	4	Q8TER1	Q8ter1 homo sapien
9	91.5	7.2	212	16	Q86312	Q86312 mycobacter
10	90.5	7.1	1100	2	Q93713	Q93713 deinococcus
11	89	7.0	522	10	Q9FHN7	Q9fhn7 oryza sativa
12	89	7.0	664	16	Q9HFT9	Q9hft9 pseudomonas
13	89	7.0	854	16	Q9FP20	Q9fp20 streptomyce
14	88	6.9	655	16	Q9fbr7	Q9fbr7 streptomyce
15	87.5	6.9	274	10	Q949L6	Q949l6 beta vulgaris
16	87	6.9	5192	2	Q93tw9	Q93tw9 stigmatella

; PRIOR FILING DATE: 2000-05-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/34755
 ; PRIOR FILING DATE: 2000-12-19
 ; PRIOR APPLICATION NUMBER: US 09/742,454
 ; PRIOR FILING DATE: 2000-12-19
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 2
 ; LENGTH: 273
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: TWEAK fusion protein construct
 US-09-810-777-2

Query Match 84.1%; Score 1066; DB 10; Length 273;
 Best Local Similarity 100.0%; Pred. No. 1.8e-89;
 Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

43 SLGSASLSQLQEPAQEEELVAEEDQDPSELENPOTESQDPAPFLNLVRPRRSAPKGRKTR 102
 67 SLGSASLSQLQEPAQEEELVAEEDQDPSELENPOTESQDPAPFLNLVRPRRSAPKGRKTR 126

Qy 103 ARRAAAHYEVHPRGQDGAQAGVGTGVSGWEARINSSPLRNYQIGEFIVTRAGLY 162
 Db 127 ARRAAAHYEVHPRGQDGAQAGVGTGVSGWEARINSSPLRNYQIGEFIVTRAGLY 186

Qy 163 LYCOVTHDEGKAVYLKDLDLVGVLAIRCLEEFSATAASSLGPOIRLCQVSGLLAALRPGS 222
 Db 187 LYCOVTHDEGKAVYLKDLDLVGVLAIRCLEEFSATAASSLGPOIRLCQVSGLLAALRPGS 246

Qy 223 SLRRTLPWHLKAAPFLTYFGLFQVH 249
 Db 247 SLRRTLPWHLKAAPFLTYFGLFQVH 273

RESULT 5 US-09-905-810-1

; Sequence 1, Application US/09905510
 ; Patent No. US20020015703A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BIOPEN, INC.
 ; APPLICANT: RENNERT, Paul
 ; TITLE OF INVENTION: Antagonists of Tweak and of Tweak
 ; TITLE OF INVENTION: Receptor and Their Use to Treat Immunological Disorders
 ; FILE REFERENCE: A068 US
 ; CURRENT APPLICATION NUMBER: US/09/905,810
 ; CURRENT FILING DATE: 2001-07-13
 ; PRIOR APPLICATION NUMBER: PCT/US00/01044
 ; PRIOR FILING DATE: 2000-01-14
 ; PRIOR APPLICATION NUMBER: 60/116,168
 ; PRIOR FILING DATE: 1999-01-15
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 1
 ; LENGTH: 225
 ; TYPE: PRT
 ; ORGANISM: Murine
 US-09-905-810-1

Query Match 80.4%; Score 1020; DB 10; Length 225;
 Best Local Similarity 88.8%; Pred. No. 2.2e-85;
 Matches 199; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

Qy 26 LGIGLALACIGLILAVVSGRASLQAQPAAEELVAEEDQDPSELENPOTESQDPAPL 85
 Db 2 LSIGLALACIGLILVWVSLGSWATLSAQPSQEELTAEERREPEPLNPOTESQDPVPL 61

Qy 86 NRLYPRRSAPKGXTRAAIAAHYEVHPRGQDGAQAGVGTGVSGWEARINSSPLR 145
 Db 62 EQLYPRRSAPKGXTRAAIAAHYEVHPRGQDGAQAGVGTGVSGWEETKNSSPLR 121

Qy 146 YNQIGEFIVTRAGLYYLCQVHDEGKAVYLKDLDLVGVLAIRCLEBFSATAASSLGP 205

RESULT 6 US-09-813-329-6
 ; Sequence 6, Application US/09813329
 ; Patent No. US20020012968A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: No. US20020012968A1 Drosophila Tumor Necrosis Factor Class Mole
 ; FILE REFERENCE: D016,np
 ; CURRENT APPLICATION NUMBER: US/09/813,329
 ; PRIOR APPLICATION NUMBER: 60/190,816
 ; NUMBER OF SEQ ID NOS: 65
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 6
 ; LENGTH: 409
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 US-09-813-329-6

Query Match 9.1%; Score 116; DB 10; Length 409;
 Best Local Similarity 25.5%; Pred. No. 0.011;
 Matches 55; Conservative 33; Mismatches 95; Indels 36; Gaps 10;

Qy 47 RASTSAQEPAQELVAE---EDQDPSELENPOTESQDPAPFLNLVRPRRSAPKGRKTR 102
 Db 208 RKRSRSIADVRNEEONIGNHTLQEKSNEATSKS--PAPLHR---RHMRSRHHL 261

Qy 103 ARRA-----IAHYEVHPRGQDGAQAGVGTGVSGWEARINSSPLRNYQIGEFIVT 156
 Db 262 VRKARSEDSPRAAHFLSSRRHGSMSYHGDMYIGNDNERNSYQG-HFQTRDGVLTVT 319

Qy 157 RAGIYLYCQV---HFDEGKAVYLKDLDLVGVLAIRCLEBFSATAASSLGP 211
 Db 320 NTGLYYVTAQICYNNNSHDONGFIVP----QGDTTPFLQCLN---TVPTNMIPHKVHTC 369

Qy 212 VSGLLAALRPGSSLIRTL--PWHLKAAPFLTYFGLFQV 248
 Db 370 TSGLIHLERNEIRHLKDINDDRNAVLREGNNSYFGIFKV 409

RESULT 7 US-09-813-329-4

; Sequence 4, Application US/09813329
 ; Patent No. US20020012968A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: No. US20020012968A1 Drosophila Tumor Necrosis Factor Class Mole
 ; FILE REFERENCE: D016,np
 ; CURRENT APPLICATION NUMBER: US/09/813,329
 ; PRIOR APPLICATION NUMBER: 60/190,816
 ; NUMBER OF SEQ ID NOS: 65
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 4
 ; LENGTH: 406
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 US-09-813-329-4

Query Match 8.3%; Score 105.5; DB 10; Length 406;
 Best Local Similarity 24.2%; Pred. No. 0.1;

Matches 54; Conservative 35; Mismatches 97; Indels 37; Gaps 10; LENGTH: 409

Query 49 SLSAEGPAQREL----VAEEDQ----DFSEL----NPQTEEQDPAFPFLNVRPR 93
 Database 198 SYNAPRKQCRKSRADIYRVEEQN1QGNHTELQKSSNEATSKERMRHRRHLLVKG 257

Query 94 SAPKGKRTRARRAIIAAHYEVHPRPGDQAGVQGDTGVSWEARINSSSPLYRNQIGEF 153
 Database 258 SLLSRSERDP--PAHFILSSRRRHQGSM--GYHCDMYGNDNERNNSYQG--HFQTRDGVL 313

Query 154 IVTRAGLYLYQCV----HFDEGKAVYLKDLLDVGVLAIRCLEEFSATAASSLGQLR 208
 Database 314 TVNTGLYYQAQICYNNNSHDQNGFIV----QGDTPFLQCLN----TVPTNMVKVH 363

Query 209 LCQVGLAARPGSSLRIRTL----PWAHLKAAFPFTYFGIFQV 248
 Database 364 TCHTSGLHLERNERIHLKDIIHNDRAVLREGNNNSYFGIFKV 406

~SULT 8
 Sequence 2, Application US/09813329
 Patent No. US2002012968A1
 GENERAL INFORMATION:
 APPLICANT: Bristol-Myers Squibb Company
 TITLE OF INVENTION: No. US2002012968A1 Drosophila Tumor Necrosis Factor Class Mole
 FILE REFERENCE: D0016 np
 CURRENT APPLICATION NUMBER: US/09/813,329
 CURRENT FILING DATE: 2001-03-20
 PRIOR APPLICATION NUMBER: 60/190,816
 PRIOR FILING DATE: 2000-03-21
 NUMBER OF SEQ ID NOS: 65
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 2
 TYPE: PRT
 ORGANISM: Drosophila melanogaster
 US-09-813-329-2

Query Match 8.2%; Score 104; DB 10; Length 409;
 Best Local Similarity 25.9%; Bred. No. 0.14; Indels 28; Gaps 10;
 Matches 56; Conservative 32; Mismatches 100; Indels 28; Gaps 10;

Query 47 RASL3QPEAELVAE----EDQPSLEINPQTEQDPAFP--IIRLVRPFRSAFKRKT 101
 Database 208 RKSRSIADYRVEEQN1QGNHTELQKSSNEATSRS--PAALHLRRMRSRRHLLVVRKA 265

Query 102 RARRA-IAAHYEVHPRPGDQAGVQGDTGVSWEARINSSSPLYRNQIGEFIVTRAGL 160
 Database 266 RSEDSPAAHFLSSRRRHQSM--GYHCDMY-IEENDRERSYQGDFQTRDGVLTVNAGL 323

Query 161 YYLYCQ----HFDEGKAVYLKDLLDVGVLAIRCLEEFSATAASSLGQLRQVSGI 215
 Database 324 YYVVAQIGWYNSHDQNGFIV----QGDTPFLQCLN----TVPTNMVKVHTCHTSGL 373

Query 216 LALRGGSSLRIRTL----PWAHLKAAFPFTYFGIFQV 248
 Database 374 IHLENERIHLKDIIHNDRAVLREGNNNSYFGIFKV 409

RESULT 9
 Sequence 39, Application US/09027287A
 Patent No. US20020064869A1
 GENERAL INFORMATION:
 APPLICANT: Ebner, Reinhard
 APPLICANT: Yu, Guo-Liang
 APPLICANT: Ulrich, Stephen M.
 TITLE OF INVENTION: Apoptosis Inducing Molecule II
 FILE REFERENCE: 1488.050004
 CURRENT APPLICATION NUMBER: US/09/252,656B
 CURRENT FILING DATE: 1999-02-19
 PRIOR APPLICATION NUMBER: US/09/0006
 PRIOR FILING DATE: 1999-02-20
 PRIOR APPLICATION NUMBER: US/09/252,656B
 PRIOR APPLICATION NUMBER: US/09/0006
 PRIOR FILING DATE: 1998-02-20
 PRIOR APPLICATION NUMBER: US/09/003,886
 PRIOR FILING DATE: 1998-01-07
 PRIOR APPLICATION NUMBER: US/08/822,953
 PRIOR FILING DATE: 1997-03-21
 PRIOR APPLICATION NUMBER: US/09/013,923
 PRIOR FILING DATE: 1996-03-22
 PRIOR APPLICATION NUMBER: US/09/030,157
 NUMBER OF SEQ ID NOS: 61
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 39
 LENGTH: 208
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-252-656B-39

Query Match 7.3%; Score 92.5; DB 10; Length 208;
 Best Local Similarity 25.0%; Pred. No. 0.62;
 Matches 41; Conservative 18; Mismatches 38; Indels 67; Gaps 7;

Qy 22 VPLA-LOGLGLA-LACGLLIAV-----VSLGSRASLSAQEPAAQELVAAEDQDPSEINPUT 75
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 1 IPRARVGLGGLLULLMGAGLAVQGMFLQLHWRLG-----EMV-----T 38
 Qy 76 EESQDPAPFLNRLVRPPLSAPKGRKTRARRAIAAHYEVHPRPGDGAQCVGDTGVSWE 135
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 39 RLPDGPGSWEQLIQERRS-----HEVNPAAHLTGANSLLTG-----T 75
 Qy 136 ARINSSSPRLYRNQI-----GEPIVTRAGLYLYCQV 167
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 76 ---SGCPLLWETOLGLAFLRGLSYHDLGALVVTKAGXXYISKV 115
 Qy RESULT 11
 US-09-967-604-6
 : Sequence 6, Application US/09967604
 : Publication No. US20030050605A1
 : GENERAL INFORMATION:
 : APPLICANT: LA JOLLA INSTITUTE FOR ALLERGY AND IMMUNOLOGY
 : TITLE OF INVENTION: LIGAND FOR HERPES SIMPLEX VIRUS ENTRY MEDIATOR AND
 : METHODS OF USE
 : FILE REFERENCE: 051501/0278793
 : CURRENT APPLICATION NUMBER: US/09/967,604
 : CURRENT FILING DATE: 2002-05-03
 : PRIORITY NUMBER: 09/549,096
 : PRIOR FILING DATE: 2000-04-12
 : PRIOR APPLICATION NUMBER: 08/698,234
 : PRIOR FILING DATE: 1997-07-30
 : PRIOR APPLICATION NUMBER: 60/051,964
 : PRIOR FILING DATE: 1997-07-07
 : NUMBER OF SEQ ID NOS: 6
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 6
 : LENGTH: 240
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 : US-09-967-604-6
 Qy Query Match 7.2%; Score 91.5; DB 9; Length 240;
 Qy Best Local Similarity 25.0%; Pred. No. 0.93; Mismatches 47; Indels 67; Gaps
 Db Matches 44; Conservative 18; Mismatches 47; Indels 67; Gaps
 Qy 5 RSRRRG-RRGEPGTALVPLAIGLGLA-LACGLLIAV-SLGSRASLSAQEPAAQELVAE 63
 Db 26 RSRRRQCSVARVGLLIL-LINGAGLAVQGWFLQLHWRLG-----EMV-- 69
 Qy 64 EDQDPSEIPLNPQTEESQDPAPFLNRLVRPPLSAPKGRKTRARRAIAAHYEVHPRGDGAQ 123
 Db 70 -----TRLPGDAGSWEQLIQERRS-----HEVNPAAHLTGAN 102
 Qy 124 AGVDGTVSGWEARINSSPLVRNQI-----GEFIVTRAGLYLYCQV 167
 Db 103 SSITG-----SGGPLLWETQGLASLRCLSHDGALUVTKAGYYIISKV 147
 Qy RESULT 12
 US-10-151-882-45
 : Sequence 45, Application US/10151882
 : Publication No. US2003009862A1
 : GENERAL INFORMATION:
 : APPLICANT: Steven M. Rubin.
 : TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL).
 : FILE REFERENCE: PFS54
 : CURRENT APPLICATION NUMBER: US/10/151,882
 : CURRENT FILING DATE: 2002-05-22
 : PRIOR APPLICATION NUMBER: 60/293,100
 : PRIOR FILING DATE: 2001-05-24
 : NUMBER OF SEQ ID NOS: 48
 : SOFTWARE: PatentIn version 3.0
 : SEQ ID NO 45
 : LENGTH: 240
 : TYPE: PRT

RESULT 13
US-09-027-287-2

Query Match
Best Local Similarity 2
Matches 44; Conservation

Qy	5	RSQRQRQC-RRQEPCGTAL	1	1	1	1	1	1	1	1	1
Db	26	RSHRRQCSVARVGLGL	1	1	1	1	1	1	1	1	1

Qy 64 EDQDPSSLNPQTEESQ

Db 70 -----TRLPDC

Qy 124 AGVDGTVSGWBEARINS

Db 103 SSSLTG-----S

RESULT 14
US-09-252-656B-2

Query Match
Best Local Similarity 2
Matches 44; Conservation

Qy	5	RSQRQRQC-RRQEPCGTAL	1	1	1	1	1	1	1	1	1
Db	26	RSHRRQCSVARVGLGL	1	1	1	1	1	1	1	1	1

Qy 64 EDQDPSSLNPQTEESQ

Db 70 -----TRLPDC

Qy 124 AGVDGTVSGWBEARINS

Db 103 SSSLTG-----S

APPLICANT: Ruben, Steven M.
 APPLICANT: Zhang, Jun
 APPLICANT: Ullrich, Stephen
 APPLICANT: Zhai, Yifan
 TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
 FILE REFERENCE: 1488 0650006
 CURRENT APPLICATION NUMBER: US/09/252,656B
 CURRENT FILING DATE: 1999-02-19
 PRIOR APPLICATION NUMBER: US 60/075,409
 PRIOR FILING DATE: 1998-02-20
 PRIOR APPLICATION NUMBER: US 09/027,287
 PRIOR FILING DATE: 1998-02-20
 PRIOR APPLICATION NUMBER: US 09/003,886
 PRIOR FILING DATE: 1998-01-07
 PRIOR APPLICATION NUMBER: US 08/822,953
 PRIOR FILING DATE: 1997-03-21
 PRIOR APPLICATION NUMBER: US 60/013,923
 PRIOR FILING DATE: 1996-03-22
 PRIOR APPLICATION NUMBER: US 60/030,157
 PRIOR FILING DATE: 1996-10-31
 NUMBER OF SEQ ID NOS: 61
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 2
 LENGTH: 240
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-252,656B-2

Query Match 7.2%; Score 91.5; DB 10; Length 240;
 Best Local Similarity 25.0%; Pred. No. 0.93; Indels 67; Gaps 7;
 Matches 44; Conservative 18; Mismatches 47; Indels 67; Gaps 7;

Qy 5 RSQRRG-RGEGPTAILVPLAIGLALACIGLILLAVSLSRASLSAQEPQAEELVAE 63
 Db 26 RSHRROSCTSVARVGLILL-LLMGAGLAVQGMFLQLHWRLG-----EMV-- 69
 Qy 64 EDQDPSELNPQTEESQDPAFPNRLVPRPSAPKGRKTRARRAIAAHYEVPRPGDGAQ 123
 Db 70 -----TRLDGPAGSWEQLIQERRS-----HEVNPAAHLTGAN 102
 Qy 124 AGVDTGTVSGWEARINSSPLRYNQI-----GEFIVTRAGLYLYCQV 167
 Db 103 SSITG-----SGGPULLWETQLGLAFLRGLSYHDGALVTKAGYYIVYSKV 147

Search completed: April 12, 2003, 08:47:28
 Job time : 18 secs

US-10-066-209-4
 Sequence 4, Application US/10066609
 Agent No. US2002011510A1
 GENERAL INFORMATION:
 APPLICANT: Brigham-Burke, Michael R.
 APPLICANT: Young, Peter R.
 TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
 TITANOIDS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
 FILE REFERENCE: GH-5030-01
 CURRENT APPLICATION NUMBER: US/110/0666,209
 CURRENT FILING DATE: 2001-10-25
 PRIOR APPLICATION NUMBER: 09/072,993
 PRIOR FILING DATE: 1998-05-06
 PRIOR APPLICATION NUMBER: 60/055,513
 PRIOR FILING DATE: 1997-08-13
 PRIOR APPLICATION NUMBER: 60/056,980
 PRIOR FILING DATE: 1997-08-16
 PRIOR APPLICATION NUMBER: 60/057,550
 PRIOR FILING DATE: 1997-08-29
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 4
 LENGTH: 240
 TYPE: PRT
 ORGANISM: HOMO SAPIENS
 US-10-066-209-4

Qy 165 -----CQVHFDEGKAVLKLDDLVGVTLARCLEEFSATAASSLGPOURLCOVS-- 213
 Db 167 DWQPGEDRPMPAHFQPEURLHL----- PSATGEQTHLSLVAPG 204

Qy 214 -----GLIALRPGSSLIRIT 228
 Db 205 PGPRDPDWLPQALATLALSGSSASRLT 232

RESULT 4
 Q93JDI PRELIMINARY; PRT; 937 AA.
 AC Q93JDI;
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Putative membrane protein.
 GN STBAC1H6.31 OR SC05996 OR SCBAC16H6.31.

Streptomyces coelicolor.
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 Actinomycetales; Streptomyces; Streptomyctaceae; Streptomyces.
 OX NCBI_TAXID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 STRAIN=A3 (2);
 RC Collins M.R.; Harris D.;
 RA Bentley S.D.; Parkhill J.; Barrell B.G.; Rajandream M.A.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3 (2);
 RX MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M.; Kieser H.M.; Denapaité D.; Eichner A.; Cullum J.,
 RA Kinash H.; Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RT Mol. Microbiol. 21:77-96(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3 (2) / M145;
 RA Bentley S.D.; Chater K.F.; Cerdeno-Tarrega A.-M.; Challis G.L.,
 RA Thomson N.R.; James K.D.; Harris D.E.; Quail M.A.; Kieser H.,
 RA Bateman A.; Brown S.; Chandra G.; Chen C.W.; Collins M.,
 RA Cronin A.; Fraser A.; Goble A.; Hidalgo J.; Hornsby T.; Howard S.,
 RA Huang C.-H.; Kieser T.; Larke L.; Murphy L.; Oliver K.; O'Neil S.,
 RA Rabbowitsch E.; Rutherford M.A.; Rutter S.; Taylor K.,
 RA Seeger K.; Saunders D.; Sharp S.; Squares R.; Taylor K.,
 RA Warren T.; Wietzorek A.; Woodward J.; Barrell B.G.; Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3 (2)." Nature 412:141-147 (2001).
 CC - SIMILARITY: CONTAINS 13 WD REPEATS (TRP-ASP DOMAINS).
 DR InterPro; IPR000408; Reg_chr_condens.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF0400; WD40_13.
 DR PROSITE; PS00626; RC1_2; UNKNOWN_1.
 DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_5.
 DR PROSITE; PS50082; WD_REPEATS_2; 9.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 SQ SEQUENCE 937 AA; F14E4478A6B6B2F5 CRC64;

Query Match 7.4%; Score 94; DB 16; Length 937;
 Best Local Similarity 25.4%; Fred. No. 9.7;
 Matches 46; Conservative 19; Mismatches 64; Indels 52; Gaps 6;

Qy 5 RSQRREGRGRGEPTALLVPLAUGLGLALAQLGLLLAVSUGSRAASLSAQP-----A 56
 Db 213 RSEGURDTRNLRLTARIVATAGCULLVAS---TLSVVAVLSSRAATRQDQAVVQQLIT 269
 Qy 57 QEELVAAEDOPPSLEINPQTESQDPA-----FLNRLVRPRRS-----APKG 98
 Db 270 QSSLLAERDPEAFLKALAARWIDSPETRFAVLDAAVNPAASVLSHVSVPDSVAFSPDG 329
 Qy 99 R-----KTRARRAAHYE-----VHPRPGDQGAQCVGTVSGWEE 135
 Db 330 RTVASSGSDGVVRWRTGTTGRTAGRPLIGHQGITSIAFAPGRTLASSGFDTVRLWDL 389

RESULT 5
 Q9RJ01 PRELIMINARY; PRT; 776 AA.
 AC Q9RJ01;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Putative cation-transporting ATPase.
 GN SC00164 OR SCU1.13.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinomycetidae;
 OC Streptomyctaceae; Streptomyceae; Streptomyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3 (2);
 RA Seeger K.J.; Harris D.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3 (2);
 RA Thomson N.R.; Parkhill J.; Barrell B.G.; Rajandream M.A.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3 (2);
 RX MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M.; Kieser H.M.; Denapaité D.; Eichner A.; Cullum J.,
 RA Kieser H.; Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RT Mol. Microbiol. 21:77-96(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3 (2) / M145;
 RA Bentley S.D.; Chater K.F.; Cerdeno-Tarrega A.-M.; Challis G.L.,
 RA Thomson N.R.; James K.D.; Harris D.E.; Quail M.A.; Kieser H.,
 RA Bateman A.; Brown S.; Chandra G.; Chen C.W.; Collins M.,
 RA Cronin A.; Fraser A.; Goble A.; Hidalgo J.; Hornsby T.; Howard S.,
 RA Huang C.-H.; Kieser T.; Larke L.; Murphy L.; Oliver K.; O'Neil S.,
 RA Rabbowitsch E.; Rutherford M.A.; Rutter S.; Taylor K.,
 RA Seeger K.; Saunders D.; Sharp S.; Squares R.; Taylor K.,
 RA Warren T.; Wietzorek A.; Woodward J.; Barrell B.G.; Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3 (2)." Nature 412:141-147 (2001).
 RL Nature 417:141-147 (2002).
 DR EMBL; AL109962; CAB53131.1;
 DR InterPro; IPR002106; AtRNA_LigaseII.
 DR InterPro; IPR001757; AtPase_E1-E2.
 DR InterPro; IPR001454; Hlgnaase/hydrolase.
 DR Pfam; PF00122; E1-E2 ATPase; 1.
 DR PRINTS; PR00119; CATAFASE.
 DR PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
 DR PROSITE; PS00154; ATPASE_E1_E2; UNKNOWN_1.

GN FLJ00093;	RA Parkhill J.; Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases [3];
OS Homo sapiens (Human);	RN Sequence FROM N.A.
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	RC STRAIN=DC 1551 / OSHKOSH;
OX NCBI_TAXID=9606;	RP Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [1];	RA "Whole genome comparison of <i>Mycobacterium tuberculosis</i> clinical and laboratory strains."
SEQUENCE FROM N.A.	RA "The nucleotide sequence of a long cDNA clone isolated from human spleen." [2];
RC TISSUE=SPLEEN;	RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RA Ohara N., Nagase T., Kikuno R., Okumura K.;	RA Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RT "The nucleotide sequence of a long cDNA clone isolated from human spleen." [1];	RA Bishai W.;
RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.	RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Kolonay J.F., Nelson W.C., Umayam L.A., Brumfitt W., Salzberg S.L., Fleischmann R.D., Allard D., Eisen J.A., Carpenter L., Haft D., Hickey E., Peterson J., DeBoy R., Dodson R., Gwynn M.L., Haft D., Brumfitt W., Umayam L.A., Brumfitt W., Salzberg S.L., Mikula A., Kolonay J.F., Nelson W.C., Umayam L.A., Brumfitt W., Salzberg S.L., Mikula A., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W.;
RL EMBL: AK074040; BAB84866.1; -.	RT "Whole genome comparison of <i>Mycobacterium tuberculosis</i> clinical and laboratory strains."
FT NON-TER 1	RA Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
SQ SEQUENCE 977 AA; 103643 MW; D9815cEA240E411 CRC64;	CC -1. SIMILARITY: BELONGS TO THE TETRACRR FAMILY OF TRANSCRIPTIONAL REGULATORS.
Query Match 7.3%; Score 92; DB 4; Length 977; Best Local Similarity 25.6%; Pred. No. 15; Gaps 13; Matches 64; Conservative 25; Mismatches 75; Indels 86; Gaps 13;	CC REGULATORS.
Db 13 RGGDTALLVPLAAGLGLACIGLILAVLVSRSASISQAPEQELVA--BEDQDPS 70	DR EMBL: 293777; CAB07841.1; -.
Db 38 RGGPG--LGGLISGAAALALP-LGLVTLGWPARGDLSPPSITSMPTLGWLPENRDSE 93	DR EMBL: AE007002; AAK45514.1; -.
Qy 71 LNQCTEEQ---DPAPEL-----NRLVPRRRSAPKGRKTRARRAIAAH-----110	DR TIGR: MT1257; -.
Db 94 DQSQAEQTOALASQASQIAKVESFERIIQAGRIMPQQVKGFQRQIAHAALEETYKA 153	DR Tuberculist: RV1219C; -.
Qy 111 -YEVHPRPGQDGQ--AGYDGTIVSGWEARINSSPRLYN-ROIGEFIVTRAGLYLYCQ 166	DR InterPro: IPR001647; HTH_TetR.
Db 154 CRRQHP-----AQPLASSKG-----PGRFDPRELEAEIYRLGSCLELK 194	DR PFM: PF00440; ttrR; 1.
Qy 167 VHEDE-----GKAVYIQLDQIIVDGYTIALRCD-----EEF 195	DR DNA-binding: Hypothetical protein; Transcription regulation;
Db 195 EHDTQOEPEPGS-----DSALDSTPAPLCHQOPTLPPAPSGQAPMPAIKTSCEPEA 248	DR Complete proteome.
Qy 196 SATASSLGP 205	DR 21 AA; 23181 MW; 8FBC3B909BA88C0 CRC64;
Db 249 TTTAAATGTP 258	DR SEQUENCE
RESULT 9	Query Match 7.2%; Score 91.5; DB 16; Length 212; Best Local Similarity 24.5%; Pred. No. 2.5; Gaps 9; Matches 53; Conservative 26; Mismatches 78; Indels 59; Gaps 9;
ID 086312 PRELIMINARY; PRT; 212 AA.	Qy 11 GFRGP GTTALLVPLAAGLGL---ALACLGILLAVVSLGSASLSAQEPADBELVAA--64
AC 086312; DT 01-NOV-1998 (TREMBLrel. 08, Created) ID Q937L3 PRELIMINARY; PRT; 1100 AA.	Db 21 GRHG-----FCVGLRAIAEAAGVSAALVHFGSEGL---RKACDDFVAEIR 66
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)	Qy 65 -----DQDPSLENPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHPR 116
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)	Db 67 SSKAAAALKSNPDTWIAQMAEAEESYAPLMAVLRVSNMISGGGLAKMLWQKML-----117
DE Hypothetical protein (Transcription regulator, TetR family).	Qy 117 PSQDGAQAGQDGTGTVSGWEEARINSSPLRNYRQIGEFL-VTRAGLYLYCQVHFD-----170
GN GN129 OR MT161_02C OR MT1257.	Db 118 ---DNAEYELD-----EGVRAGTVKPSRDRARARFLATGGGGFLLYLQMHENPTDLR 168
OS Mycobacterium tuberculosis.	Qy 171 -----EGKAVYIQLDQIIVDGYTIALRCD-----199
OC Bacteria; Firmicutes; Actinobacteria; Actinomycetidae; Actinomycetales; Corynebacterineae; Mycobacterium.	Db 169 AALRDYAHDMVLPSSLEVYEGTGLLADRMYEFLAEA 204
NCBI_TAXID=1773;	Qy 172 -----EGKAVYIQLDQIIVDGYTIALRCD-----199
RN	DB Deinococcus radiodurans.
RP	OC Deinococcaceae; Deinococcus group; Deinococci; Deinococcales;
RC STRAIN=H37RV;	OC Deinococcaceae; Deinococcus.
RX MEDLINE:98295987; PubMed=9634230;	NCBI_TAXID=1299;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gaidatzis S., Gaidatzis S., Helliwell J., Hornsby T., Jagels K., Krogh A., McLean J., Moules S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;	OX
RT "Deciphering the biology of <i>Mycobacterium tuberculosis</i> from the complete genome sequence." [2];	RN Sequence FROM N.A.
RT RL Nature 393:537-544 (1998).	RP SEQUENCE FROM N.A.
RN	RA "Phylogenetic analysis of SMC proteins." [1];
RC STRAIN=H37RV;	RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

Best Local Similarity 26.7%; Pred. No. 24; Matches 5; Conservative 23; Mismatches 73; Indels 55; Gaps 8;	ID Q9HYT9 PRELIMINARY; AC Q9HYT9; DT 01-MAR-2001 (TREMBLrel. 16, Created) DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update) DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update) DE Hypothetical protein PA3305.
50 LSAQEPAA---QELVAAEDQDPSELNPQTEESQDPAPFLNRLVRPQRSAPKGRL----- 99	OS Pseudomonas aeruginosa.
698 LSAQTRSLRSHRDLTARLERDARLRLPVPTEDATDPAELESALWQAROQAEETGAAEERA 757	OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaeae; OC Pseudomonas.
100 -----KT-RARRAIAHVEVHPRPQDGAA---QKCVD-----G 128	NCBI_TaxID=287;
758 LEALALARELDTAKTYRAEARRAALRERLRYVNAQGQGLDAAAEEVARREAALG 817	OX
Qy 129 TVSGWEARINS---SSPLQYRQIGEFITVTRAGLYLQLCQVHDEGAVYLKDLYVG 185	RP SEQUENCE FROM N.A.
Db 818 TLDDQEPFPRAEAAREAAALAYANLIGEQNKVGRGFLDLRVLIAREGSA---EPIPDG 872	RC SPAIN-ATCC 15692 / PA01; RX MELLINE-2043/337; Published=10984043; RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P.M., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Gooley L., Tolentino E., Westbrook-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., RA Reizer J., Sauer M.H., Hancock R.E.W., Lory S., Olson M.V., RA "Complete genome sequence of <i>Pseudomonas aeruginosa</i> PAO1, an opportunistic pathogen." DR EMBL; AE004753; AAC06633.1; Nature 406:559-564 (2000).
Qy 186 VLALRCLEEFSAASS-----LGP 205	DR EMBL; AE004753; AAC06633.1; Hypothetical protein; Complete proteome.
Db 873 CSPPGTPKWTAAELARARAEFLDRRGP 898	KW Matches 70; Conservative 26; Mismatches 109; Indels 64; Gaps 10; SEQUENCE 664 AA; 73136 MW; 1988BF3098D1F4E CRC64;
Qy .SOUT 11 .FRTN7 PRELIMINARY; PRT; 522 AA.	Query Match Score 89; DB 16; Length 664;
AC Q9FTN7; DT 01-MAR-2001 (TREMBLrel. 16, Created) DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update) DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update) DE Putative Rer1A Protein (ATRERIA).	Best Local Similarity 26.0%; Prd. No. 18; Matches 70; Conservative 26; Mismatches 109; Indels 64; Gaps 10; SEQUENCE 664 AA; 73136 MW; 1988BF3098D1F4E CRC64;
GN P0005A05_12.	Qy 10 RGRGEPTAALVPLAIGLGLNACLGLLAVLGSRASLSAQAQEEL-----LVAE 63
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; OC Spermatophyta; Magnoliophyta; Liliopsida; Oryzae; Oryza.	DR 224 RGRRAGALLLSRDLLSL-----LRTARGVARQRARSEEERVERWLAALASAL 275
OC Enthartoidea; Oryzeae; Oryza.	Db 64 EDDDPSELNIPQTEESQDPAPFLNRLVPPRASAPKGRKTRARBAIAAHYVHPRGDQGAQ 123
NCBI_TaxID=4530; RN	Qy 64 EDDDPSELNIPQTEESQDPAPFLNRLVPPRASAPKGRKTRARBAIAAHYVHPRGDQGAQ 123
RP SEQUENCE FROM N.A.	DR 276 EGDPAQMQLAREELAQA-----VEPQNSNDQ-KYLTCSVLLJKAVN-----AE 321
RC STRAIN=CV. NIPPONBARE; RA Sasaki T., Matsumoto T., Yamamoto K.; RT "Oryza sativa nipponbare (GA3)" genomic DNA, chromosome 1, PAC clone:P0005A05_12; Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.	Qy 124 AGDGTYSGWEEARINSSPRLYNR---QIGEVITVTRAGL-----YYLY 164
RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.	DR 322 KGMRVAVSGEVGRVSGATGSLWHRDQMLAFLPYGTRSALALIGLSVWVITPAASGM 381
RL AP02863; BAB1690_8.1; InterPro: IPR049322; Rer1.	Qy 165 -----CQVHFDEGKAYLKLDDLVGVLARCLEEFESATASSLGQLRCQVSG-----LL 216
DR InterPro: IPR049322; Rer1; 1.	Db 382 LIAAVVCSLFAIRDNAVAYAIGSFLRGIVYAI-----PAAMLYSQWLIPQWNGFPPLL 432
SG SEQUENCE 522 AA; 58171 MW;	Db 433 *CLAMGVBPBFATGMAVPVTAATFATPSAI 461
Qy 47 RASLSAQ---EPADPELV-AEEQDPSELNQPEEES-QDPAP-----FLN--- 86	RESULT 13
93 RVSTVNAQRKRKERKHEEIVTSAKURGGGTIVRKRKESKEQDPGPIQHQFOQSYENTHA 152	Q9F2P0 PRELIMINARY; AC Q9F2P0; DT 01-MAR-2001 (TREMBLrel. 16, Created) DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update) DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update) DE putative ABC transport system integral membrane protein.
87 -----RVRPQR-----SAPKGKTRARR 105	Db 153 SGKAKVTVHACTVLSKDTSSRREREGREHRPASHLIGIGIVLVLGQSSKGREGFAR 212
Qy 106 AIAAHVEVHP---RPG---QNGA-----EARINSSSSPRLYNRQ 149	GN SC03110 OR SCE41.19C.
Db 213 EVVA---SPSGFRQFSMGAADSGTAGAAAAKWRTDASRFQYYDRSTHATGRW 268	OS Streptomyces coelicolor.
Qy 150 IGEFLVTRAGLYLYCQVHDE-----GKAVVTKLIDLVGVLARCLEEFESATASS 202	OC Bacteria; Firmicutes; Actinobacteria; Actinomycetaceae; Streptomyces.
269 IGTAVV-AAYAL---RVLVQGFIYIVTGLIVL-LNLLI-GTSPMVDEPEAK-AASS 321	OC Actinomycetales; Streptomyceae; Streptomyces.
203 LGPQDLRLCQVSGLGLAURPGSSLRFLRLP---WHLKA---APFLTYGLFQV 248	NCBI_TaxID=1902;
322 DGPAL---PTRGSDDFKPL---FTRLPEPKWMAITRFLIAFPMTFSVFDY 368	RN [1] SEQUENCE FROM N.A.
Db	RP STRAIN=3 (2); RC Saunders D.C., Harris D.; RA Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
RESULT 12 Q9HYT9	RL [2] RN [2] SEQUENCE FROM N.A.

RC	STRAIN=A3 (2);	RA	Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA	Cerdillo A.M., Parkhill J., Barrell B.G., Rajandream M.A., Rajandream M.A., Submitted (SBP-2000) to the EMBL/GenBank/DBJ databases.	RA	Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutten S.,
RL	[3]	RA	Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RN	SEQUENCE FROM N.A.	RA	Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,
RP	SEQUENCE FROM N.A.	RA	Hopwood D.A.;
RC	STRAIN=A3 (2);	RT	"Complete genome sequence of the model actinomycete Streptomyces
RC	MEDLINE=97000351; PubMed=8843436;	RT	coelicolor A3(2)";
RX	Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J., Kieser H.M., Hopwood D.A.;	RT	Nature 417:141-147 (2002).
RA	"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";	DR	EMBL; AJ391588; CAC04433.1;
RT	RL Mol. Microbiol. 21:77-96 (1996).	SQ	SEQUENCE 655 AA; 67324 MW; 523242CDF3B7F109 CRC64;
RN	[4]	Query Match	6.9%; Score 88; DB 16; Length 655;
RP	SEQUENCE FROM N.A.	Best Local Similarity	24.2%; Pred. No. 21;
RC	STRAIN=A3 (2) / M145;	Matches	56; Conservative 15; Mismatches 52; Indels 108; Gaps 12;
RA	Bentley S.D., Chater K.F., Cerdillo-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harmer D., Bateman A., Brown S., Chanda G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutten S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J., Hopwood D.A.;	Qy	28 LGIALAIC----GLILIA-----VVSIGSRASLSAQEPQAEELV--AEEEDD- 67
RA	"Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2)." ;	Db	34 LGALVCAADPAUSGVILVLDPLVPARLFGAVLAGAAEPARPLVLGASDRDELDL 93
RT	Nature 417:141-147 (2002).	Qy	68 -----PSELNPQTE-ESODPAPEL-----
DR	EMBL; AJ39120; CAC09551.1. -.	Db	94 WTRIRGEGHGTIVRTEPGPLTEGGDADGAPPVYVYDARLSVAGMRAAYQLLGADVV 153
DR	InterPro: IPR003838; DUF214. 2.	Qy	86 -----NRLVVR-----RSAPKGKTR-----ARRAIAAHY 112
DR	PFam: PF02687; DUF214. 2.	Db	154 TVERGGPRTVRPRPARWILAVCRSADVGRVSRHLLDFAVRLSAGLRLPGVREALA--E 210
SQ	SEQUENCE 854 AA; 89272 MW; DED07C6D3ABAFA57 CRC64;	Qy	113 VHPRGDQGAQAG-----VDTGTVSGWEARINSSPLRNYRQIGEFIVTRA 158
Query Match	7.0%; Score 89; DB 16; Length 854;	Db	211 TGRP-EAGAAGGEAFLPAGLPAAMRSAAGGVRPV---PVGDAAGIGRA 256
Best Local Similarity	21.8%; Pred. No. 24;	RESULT 15	SEQUENCE FROM N.A.
Matches	39; Mismatches 81; Indels 34; Gaps 8;	Q949L6	Q949L6 PRELIMINARY;
Qy	1 MAARSQRGRGRGEPGTALLPVALGLGLACIGLIAVVSIGRSRASLSAQEPQAEEL 60	AC	Q949L6 PRELIMINARY;
Db	482 LAERNALANPRTGATGALMIGAL---WQASLVSIGS--SIVASATSELDITVGADF 534	DT	01-DEC-2001 (TREMBLrel. 19, Created)
Qy	61 VAEDQDPSELNPQTEESQDPAPPLNRLVPRP----RSAPKGKTRARRATAAAYHEVHP 115	DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
Db	535 IVQGNQ----RIVPAEAKMTNTPELEHTRYKVLDATUTSPDG-KTDDDGVTAA---DP 586	DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
Qy	116 RPGDGRQAGVQDGTIVS--GWEERARINGSSPLRNYRQGEFIFTAGWYLICQVHDFBG 172	DE	Putative calpain inhibitor like protein.
Db	587 TYAEDVRAETTGEGLSAAAGTGTAMSVGSDYAERKGVHGDIV-----SVAPKGG 635	OS	Beta vulgaris.
Qy	173 KAVYKLDDILVDEGVTLA 189	OC	Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.
Db	636 ETAKVKAATSDDVAI 652	OC	NCBI_TAXID=161934;
RP	SEQUENCE FROM N.A.	RN	RN [1]
RA	Kloos D.U., Oltrmanns H., Dock C., Stahl D., Hehl R.;	RA	RA
RT	"Isolation and molecular analysis of novel taproot expressed genes from sugar beet".	RT	RT
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.	DR	DR EMBL; AJ309174; CAC43296.1. -.
SQ	SEQUENCE 274 AA; 28636 MW; 4A7A16D6F496COCE CRC64;	Qy	99 RTRRAIAAHYEVIPRGDGAQGVGD 128
Query Match	6.9%; Score 87.5; DB 10; Length 274;	Db	142 EHQAAEQPAPVAERPAAPAAPIADG 171
Best Local Similarity	28.9%; Pred. No. 8;	RESULT 14	SEQUENCE FROM N.A.
Matches	12; Mismatches 43; Indels 9; Gaps 2;	Q9FBR7	Q9FBR7 PRELIMINARY;
AC	09FB7; PRELIMINARY;	AC	09FB7 PRELIMINARY;
DT	01-MAR-2001 (TREMBLrel. 16, Created)	DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)	DT	01-JUN-2001 (TREMBLrel. 21, Last annotation update)
DE	Putative ion chelatase.	DE	Putative ion chelatase.
GN	SC05278 OR SCGB12_02.	GN	SC05278 OR SCGB12_02.
OS	Streptomyces coelicolor.	OS	Bacteria; Firmicutes; Actinobacteria; Actinomycetidae; Streptomyces.
OC	Actinomycetales; Streptomycineae; Streptomyctaceae; Streptomyces.	OC	Actinomycetales; Streptomycineae; Streptomyctaceae; Streptomyces.
RN	[1]	RN	NCBI_TAXID=1902;
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RC	STRAIN=A3 (2) / M145;	RC	STRAIN=A3 (2) / M145;
RA	Bentley S.D., Chater K.F., Cerdillo-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chanda G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,	RA	Bentley S.D., Chater K.F., Cerdillo-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chanda G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Search completed: April 12, 2003, 08:40:50
Job time : 38 secs

CC tissue for successful grafting and to promote tissue grafts.
 CC The present amino acid sequence is human TREPA fragment.
 XX

SQ Sequence 146 AA:

Query Match 60.0%; Score 761; DB 22; Length 146;
 Best Local Similarity 100.0%; Pred. No. 1e-68;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SQ 1.04 RRAIAAHYEVHPRPGDQDGAQAGYDGTSGWEARINSSPLYNRQIGEFIVTRAGLYYL 163
 Db 1 RRAIAAHYEVHPRPGDQDGAQAGYDGTSGWEARINSSPLYNRQIGEFIVTRAGLYYL 60
 Qy 164 YCQVHFDEGKAYTLKLDLVDGSVLAIRCLEEFSATAASSLGQLRQCQVSGLLALRGSS 223
 Db 61 YCQVHFDEGKAYTLKLDLVDGSVLAIRCLEEFSATAASSLGQLRQCQVSGLLALRGSS 120
 Qy 224 LRIRTLPRAHLKAKAPFLTYFGLFQVH 249
 Db 121 LRIRTLPRAHLKAKAPFLTYFGLFQVH 146

search completed: April 12, 2003, 08:39:00
 Job time : 38 secs

sporulation genes";
Microbiology 142:103-3111(1996).

(2) SEQUENCE FROM N.A.

STRAIN=16-8;

MEDLINE=98044033; PubMed=9384377;

RT RN

SEQUENCE FROM N.A.

RC STRAIN=16-8;

RX MEDLINE=98044033; PubMed=9384377;

RA Kunst F., Ogasawara N., Mosser I., Albertini A.M., Alloni G.,

Azevedo V., Bertero M.G., Besieries P., Bolotin A., Borchart S.,

Boriss R., Bourlier L., Braun M., Brignell S.C., Bron S.,

Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

Denizot F., Devine K.M., Dusterhoff D., Ehrlich S.D., Emmerison P.T.,

Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

Guiseppi G., Guy B.J., Haeich J., Harwood C.R., Henaut A.,

Hilbert H., Hollsappel S., Hoono S., Hullio M.P., Itaya M., Jones L.,

Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,

Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Nobick M.,

Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,

Pohl T.M., Portebois D., Porwollik S., Prescott A.M.,

Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,

Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,

Sato T., Scanian E., Schleicher S., Schroeter R., Scuffone F.,

Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,

Sorokin A., Tocconi E., Takagi T., Takahashi H., Takemaru K.,

Takeuchi M., Tamaki A., Tanaka T., Terpstra P., Tognoni A.,

Tosato V., Uchiyama S., Vandembol M., Vannier P., Vassarotti A.,

Viani A., Wambutt R., Wedler E., Wedler H., Weitzneger T.,

Winters P., Wipat A., Yamamoto K., Yamamoto K., Yata K.,

Yoshida K., Yoshioka H.F., Zumstein E., Yoshioka H., Danchin A.,

RT "The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*";

RL Nature 390:249-256(1997).

CC EMBL: D84432; BAA12474.1; -.

EMBL: Z99117; CAB14479.1; -.

Subtilist; BG11652; Ygfb.

KW Hypothetical protein; Transmembrane; Complete proteome.

PT TRANSMEM

SQ SEQUENCE 139 AA: 15740 MW: 60C7F38CD81F4CB7 CRC64;

Query Match 6.8%; Score 86; DB 1; Length 139;

Best Local Similarity 27.8%; Pred. No. 1.6;

Matches 30; Conservative 18; Mismatches 46; Indels 14; Gaps 3;

33 ACLGILIAVVSLSGRASLQAQPQQEELVAEEDQDPSLNPOTEESQD--PAPFLNRLVR 90

13 AIGITISAIFGKKS-----EIKQNSQKRKPKHQQSASFQKQSKEDAPAPINPRMVQ 66

91 PRRSAFKGRKTRAR-----RAIAAHYEVHPRPGQDGAQGVGDTGYSG 132

67 ARREAEERRTARNLKGLERDAAKQKTVYTKQKMLQVNKDTVYQG 114

DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lymphtoxin-alpha precursor (LT-alpha) (TNF-beta) (Tumor necrosis
 DE factor ligand superfamily member 1).
 GN LTA OR TNFSF1 OR TNFB.
 OS Oryctolagidae (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagidae.
 NCBI_TAXID=9386;
 RN [1]
 RP SEQUENCE FROM N.A.; PubMed=2249779;
 RX MEDLINE=91165534;
 RA Shakhov A.N.; Kuprash D.V.; Azizov M.M.; Jongenseel C.V.,
 Nedospasov S.A.;
 RT "Structural analysis of the rabbit TNF locus, containing the genes
 encoding TNF-beta (lymphotxin) and TNF-alpha (tumor necrosis
 factor).";
 RT Gene 95:215-221(1990).
 RN [2]
 RP SEQUENCE FROM N.A.; PubMed=2613043;
 RX MEDLINE=90220566;
 RA Shakhov A.N.; Kuprash D.V.; Turetskaya R.L.; Azizov M.M.,
 Andrejeva A.V.; Nedospasov S.A.;
 RT "Cloning and structural analysis of genes coding for tumor necrosis
 factor and lymphotxin in rabbits";
 RT Mol. (Mosk) 23:1743-1750 (1989).
 RL [3]
 CC FUNCTION: Cytokine that in its homotrimeric form binds to TNFRSF1A/TNFR1, TNFRSF1B/TNFB and TNFRSF14/HVEM. In its
 heterotrimeric form with LTB binds to TNFRSF3/LTB.
 CC Lymphotxin is produced by lymphocytes and cytotoxic for a wide range of tumor
 CC cells in vitro and in vivo.
 CC SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one
 CC LTA subunits or (less prevalent) two LTA and one LTB subunits (By
 CC similarity).
 CC SUBCELLULAR LOCATION: Secreted (homotrimer) and type II membrane
 protein (heterotrimer) (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; M63454; CAA339275.1; ALT SEQ.
 DR EMBL; M63340; AAA33483.1; -.
 DR EMBL; M63041; AAA33485.1; -.
 PIR; JH0309; JH0309.
 PIR; PN0098; PN0098.
 DR HSSP; P01374; LTNR.
 DR InterPro; IPR003636; TNF abc.
 DR Inter-Pro; IPR000478; TNF family.
 DR PFam; PF00229; TNF_1.
 DR PRINTS; PR01234; TNFRSFCT.
 DR ProDom; P0002012; TNF abc; 1.
 DR SMART; SM00207; TNF_1.
 DR PROSITE; PS50049; TNF_2; 1.
 DR Cytokine; Glycoprotein; Cytotoxin; Signal.
 FT SIGNAL_1 26 LYMPHOTOXIN-ALPHA.
 FT CHAIN_27 197 LYMPHOTOXIN-ALPHA.
 FT CARBOHYD_88 98 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 197 AA; 21126 MW; 0CF18CC90B5E2345 CRC64;

Query Match Score 97; DB 1; Length 197;
 Best Local Similarity 23.7%; Pred. No. 1.9; Gaps 11;
 Matches 61; Conservative 24; Mismatches 82; Indels 90;

Qy 16 PGTALIVPLAQLGLALACUGLAVLSSRSRSLAQP-----AQEBLVAEEBDQDPS 69
 Db 3 PPGRLXPL-----LGILLAPPAPPQGAQQLGAEFFPSAARNAQQRLL-QKHFQHGS 34

Qy 70 EINPQTEESQDPAPFLNRLVPRRSAPKGRKTRAR-RAIAYHEVHPRPGQDGAQAGVGD 127
 Db 52 TIKPAAHLVGDP-----SQDSLWRANTDRAFRH----- 82;
 Qy 128 GTVSGMEEARINSSPLRNYRQIGEFTVTRAGLYYDQCQFED-EG---KAVYKLKDLLV 183
 Db 83 -----GFSLSNNSSLVPSSGLYFYSQVTSQFSGECSCSPKAVPTPLAH 125
 Qy 184 DGVLALRCLEFSA-----TAASSL-----GFLQLRQVSGNLLRGESSRIRTL 229
 Db 126 E-----VQFQSSQSFHVPLLSAQRSVCCGPQGBWRSVYQGAVFLLTQDQLSTHTD 178
 Qy 230 PWAHLKRAPFLTYFGLF 246
 Db 179 GIAHLLSPSSVFFGAF 195

RESULT 11
 TNFB_BOVIN STANDARD; PRT; 204 AA.
 ID TNFB_BOVIN
 AC 006600;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lymphotxin-alpha precursor (LT-alpha) (TNF-beta) (Tumor necrosis
 DE factor ligand superfamily member 1).
 GN LTA OR TNFSF1 OR TNFB.
 OS Bos taurus (Bovine).
 OC Bivalvia; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovine; Bos.
 NCBI_TaxID=9813;
 OX [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=94083525; PubMed=8260599;
 RA Cluds I.; Cleuter Y.; Kettmann R.; Burny A.; Droogmans L.;
 RT "Cloning and characterization of the tandemly arranged bovine
 lymphotxin and tumour necrosis factor-alpha genes.";
 RL Cytokine 5:336-341(1993).
 CC FUNCTION: Cytokine that in its homotrimeric form binds to TNFRSF1A/TNFR1 and TNFRSF14/HVEM. In its
 CC heterotrimeric form with LTB binds to TNFRSF3/LTB.
 CC Lymphotxin is produced by lymphocytes and cytotoxic for a wide range of tumor
 CC cells produced by lymphocytes and cytotoxic for a wide range of tumor
 CC cells in vitro and in vivo.
 CC -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one
 CC LTA subunits or (less prevalent) two LTA and one LTB subunits (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and type II membrane
 CC protein (heterotrimer) (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and type II membrane
 CC protein (heterotrimer) (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; Z14137; CAA78510.1; -.
 DR HSSP; P01374; LTNR.
 DR InterPro; IPR003636; TNF abc.
 DR Inter-Pro; IPR000478; TNF family.
 DR PFam; PF00229; TNF_1.
 DR PRINTS; PR01234; TNFRSFCT.
 DR ProDom; P0002012; TNF abc; 1.
 DR SMART; PS00251; TNF_1.
 DR PROSITE; PS50049; TNF_2; 1.
 DR Cytokine; Glycoprotein; Cytotoxin; Signal.
 DR EMBL; Z14137; CAA78510.1; -.
 DR HSSP; P01374; LTNR.
 DR InterPro; IPR003636; TNF abc.
 DR Inter-Pro; IPR000478; TNF family.
 DR PFam; PF00229; TNF_1.
 DR PRINTS; PR01234; TNFRSFCT.
 DR ProDom; P0002012; TNF abc; 1.
 DR SMART; PS00251; TNF_1.
 DR PROSITE; PS50049; TNF_2; 1.
 DR Cytokine; Glycoprotein; Cytotoxin; Signal.
 DR SIGNAL_1 33 BY SIMILARITY.
 DR FT 34 204 LYMPHOTOXIN-ALPHA.

prefrentially expressed in brain.";

[3] RL SEQUENCE FROM N.A. (ISOFORM JIP-1B), AND CHARACTERIZATION.

RP TISSUE:Brain; MEDLINE:2017638; PubMed=1012612;

RC RX MEDLINE:9422004; PubMed=10490659;

RA Yasuda J., Whitmarsh A.J., Cavanagh J., Sharma M., Davis R.J.;

RA "The JIP group of mitogen-activated protein kinase scaffold proteins,"

RT RT proteins,"

RL Mol. Cell. Biol. 19:7245-7254 (1999).

[4] RN TISSUE SPECIFICITY, AND SUBCELLULAR LOCATION.

RP MEDLINE:2017638; PubMed=1012612;

RC RX Gotchardt M., Tronmsdorff M., Nevitt M.F., Shelton J.,

RA Richardson J.A., Stockinger W., Nimpf J., Herz J.;

RA "Interactions of the low density lipoprotein receptor gene family with cytosolic adaptor and scaffold proteins suggest diverse biological functions in cellular communication and signal transduction.";

RT RT

RL Eur. J. Neurosci. 12:621-632 (2000).

[5] RN INTERACTION WITH LRPB.

RP MEDLINE:20400498; PubMed=10827173;

RC RX Whitmarsh A.J., Kuan C.-Y., Kennedy N.J., Kelkar N., Haydar T.F.,

RA Mordes J.P., Appel M., Rossini A.A., Jones S.N., Flavell R.A.,

RA Rakic P., Davis R.J.;

RT "Requirement of the JIP1 scaffold protein for stress-induced JNK activation.";

RT GENES Dev. 15:2421-2432 (2001).

[6] CC -!- FUNCTION: The JNK-interacting protein (JIP) group of scaffold proteins selectively mediates JNK signaling by aggregating specific components of the MAPK cascade to form a functional JNK signaling module. JIP1 is required for JNK activation in response to excitotoxic stress. Cytoplasmic JIP1 causes inhibition of JNK-activating kinase 2 (JNK2) gene expression and beta-cell function (By similarity). Appears to have a role in cell signaling in mature and developing nerve terminals.

CC -!- SUBUNIT: Forms homo- or heterooligomeric complexes. Binds specific components of the JNK signaling pathway namely JNK, MAPK7 and MLK2. MLK3 and DLX. Also binds the proline-rich domain-containing splice variant of apolipoprotein E receptor 2 (ApoE2). Binds the TPR motif-containing C-terminal of kinesin light chain. Interacts, via the PID domain, with rhoGEP (By similarity). Binds the cytoplasmic tails of LRP1 and LRP2 (Megalin).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Accumulates in cell surface projections. Under certain stress conditions, translocates to the perinuclear region of neurons. In insulin-secreting cells, detected in both the cytoplasm and nucleus (By similarity).

CC -!- ALTERNATIVE PRODUCTS: 5 isoforms: JIP1a/1, JIP1b (shown here), JIP1c/2a, JIP1d/2B and JIP1e/3; are produced by alternative splicing.

CC -!- TISSUE SPECIFICITY: Expressed predominantly in the brain and insulin-secreting cells. In the brain, high expression is found in the cerebral cortex and hippocampus. Localizes in the synaptic regions of the olfactory bulb, retina, cerebral and cerebellar cortex and hippocampus. Also expressed in a restricted number of axons, including mossy fibers from the hippocampal dentate gyrus, soma, dendrites and axons of cerebellar Purkinje cells. Also expressed in kidney, testis and prostate. Low levels in heart, ovary and small intestine. Isoform JIP-1b is more predominant in the brain than isoform JIP-1a. JIP1-a is expressed both in the brain and kidney, isoforms JIP-1C, JIP-1d and JIP-1e are brain specific.

CC -!- DEVELOPMENTAL STAGE: Low levels at prenatal stage E15, increased levels during the first postnatal days, with a plateau at postnatal day 15.

CC -!- INDUCTION: Upon neuron differentiation.

CC -!- PM: Phosphorylated by JNK in differentiated cells.

CC -!- SIMILARITY: BELONGS TO THE JIP SCAFFOLD PROTEINS FAMILY.

CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

CC -!- SIMILARITY: CONTAINS 1 PID DOMAIN.

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CC DR EMBL; AF003115; AAB65317; 1 / -;

CC DR EMBL; AF109768; AAD38346; 1 / -;

CC DR EMBL; AF109769; AAD38347; 1 / -;

CC DR EMBL; AF109770; AAD38348; 1 / -;

CC DR EMBL; AF109771; AAD38349; 1 / -;

CC DR EMBL; AF054611; AAD22580; 1 / -;

CC DR TRANSAC: T04468; -;

CC DR MGD; MGI:1309466; Prtknlp

CC DR InterPro: IPR000050; PID domain.

CC DR InterPro: IPR000452; SH3.

CC DR Pfam; PF00018; SH3; 5.

CC DR Pfam; PF00640; PID; 5.

CC DR ProDom; PD000065; SH3; 1.

CC DR SMART; SM00326; SH3; 1.

CC DR PROSITE; PS001179; PID; 1.

CC DR PROSITE; PS50002; SH3; 1.

CC KW SH3 domain; Alternative splicing; Phosphorylation.

CC FT DOMAIN 41 47

CC FT DOMAIN 107 116

CC FT DOMAIN 127 281

CC FT DOMAIN 355 359

CC FT DOMAIN 484 545

CC FT DOMAIN 557 696

CC FT VARSPLIC 1 33

CC FT VARSPLIC 69 90

CC FT VARSPLIC 69 93

CC FT VARSPLIC 558 604

CC FT VARSPLIC 144 145

CC FT VARSPLIC 593 593

CC SQ SEQUENCE 707 AA; 274013B12D91049D CRC64;

Query Match 7.1%; Score 90; DB 1; Length 707;

Best Local Similarity 26.5%; Pred. No. 4.9;

Matches 40; Conservative 16; Mismatches 59; Indels 36; Gaps 6;

Oy 29 GLALAC---LQL---LIAAVSLGSRASLQAQEPAEQELV-----AEDQD--- 67

Db 56 GTSLSQKDTLSLPRPRAGLSSGSSAGSRQLQMLIDAAGDTPQEAEDDEEDD 115

Oy 68 ---PSEIUNQTEESQDPAFPFLNVRPRRSAP---KGRKTRARRAIAHYEYHPRPG 118

Db 116 ELAAQRPGVGPKAESNQDPAP----RQGQGPGTGSQDGYRPKRPTLNFFQVPRS 169

Oy 119 QDGAQGVQDGVSGWEEARINSSPLRYNQ 149

Db 170 QDTLNNSLGGKHSQDVRVRSRSSPLKGEQ 200

RESULT 10

ID TNFB_RABIT STANDARD;

AC P1015;

DT 01-MAR-1989 (Rel. 10, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

GenCore version 5.1.4.p5 4578
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OM protein - protein search, using SW model

Run on: April 12, 2003, 08:38:14 ; Search time 20 Seconds
(without alignments)
1196.874 Million cell updates/sec

Title: US-09-905-810-2
Perfect score: 1268
Sequence: 1 MAARRSQRGGRRGGPGTAL..... PWAHIIKAAAPPLTYFGLFQVH 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext. 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR:73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: mRNA
A: Cross-references: RNBL:U03398; NID:9571322; PIDN:AAA5134.1; PID:9571323
A: Residues: 1-254 <RES>

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	91.5	7.5	254	2	A75247	4-1BB ligand - human
2	92	7.5	375	2	A75264	hypothetical protein
3	93.5	7.4	776	2	T36946	probable cation-transporter
4	93.5	7.4	1657	2	T4538	hypothetical protein
5	93	7.3	378	2	H8733	HlyD family secretory
6	91.5	7.2	212	2	A70611	hypothetical protein
7	90	7.1	441	2	S41710	mitosis-specific C
8	89	7.0	660	2	T03038	probable inhibitor
9	89	7.0	664	2	D83231	hypothetical protein
10	87	6.9	197	1	JH0309	tumor necrosis factor
11	87	6.9	204	1	S2441	lymphotoxin - bovine
12	87	6.9	310	2	D70745	hypothetical protein
13	87	6.9	445	2	T30504	hypothetical protein
14	86.5	6.8	755	2	B75346	probable competence
15	86.5	6.8	762	2	E98121	hypothetical protein
16	86.5	6.8	764	1	S41113	1-Phosphatidylinositol
17	86.5	6.8	810	2	D95256	ATP-dependent Clp
18	86	6.8	139	2	B69553	hypothetical protein
19	86	6.8	878	2	T17245	N-methyl-D-aspartate
20	86	6.8	1323	2	S27224	hypothetical protein
21	85	6.7	431	2	T01557	Glycoprotein B
22	84.5	6.7	933	1	B48319	Glycromycin synth
23	84.5	6.7	9375	2	T14593	ribosomal protein
24	84	6.6	260	2	T45750	outer surface protein
25	84	6.6	274	2	S71527	probable two-component
26	84	6.6	566	2	T3503	Glycoprotein B
27	83.5	6.6	885	1	VGBES1	probable membrane
28	83	6.5	206	2	T34961	dethiobiotin synth
29	83	6.5	228	2	B83583	Deinococcus radiodurans R1.

RESULT 1

I38427

4-1BB ligand - human

C:Species: Homo sapiens (man)

C:Date: 29-May-1998 #text_change 29-May-1998 #text_change 21-Jul-2000

C:Accession: I38427

R.Alderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.; Eur. J. Immunol. 24, 219-227, 1994

A:Title: Molecular and biological characterization of human 4-1BB and its ligand.

A:Reference number: 138426; PMID:94374434; PMID:8088337

A:Accession: I38427

A:Residues: 1-254 <RES>

A:Cross-references: RNBL:U03398; NID:9571322; PIDN:AAA5134.1; PID:9571323

Query Match 7.5% ; Score 95.5 ; DB 2 ; Length 254 ;

Best Local Similarity 25.7% ; Pred. No. 1-2 ; Mismatches 31 ; Indels 73 ; Gaps 11 ; Matches 66 ; Conservative

Qy 19 ALVPLALGLGLALCLGLLAVVSL-GSRASL-SAQEPASQSEELVQDQDSEELNPQTE 76
Db 30 ALVAGLILLLILLLAAACAVFLACPWVSGARSPGSASPRRE-----GPELSP----8
Qy 19 ALVPLALGLGLALCLGLLAVVSL-GSRASL-SAQEPASQSEELVQDQDSEELNPQTE 76
Db 30 ALVAGLILLLILLLAAACAVFLACPWVSGARSPGSASPRRE-----GPELSP----8
Qy 77 ESDQDPAPFLNLVRPRRSAPPKRKTRARRATAAAHYEVHPRPGQDGQAQGVNGTVSGWEE-135
Db 79 -DDPGLLDI-----ROGMFAQLVAQNVL-----TGPLMSYSDP 113
Qy 136 --ARINSSSPRYNRQIGEFVTRAGLYLYCQVHDEGKAVYLKLDLYVG-----VL 187
Db 114 GLAGVSUTGGLSYKEDTKEVYAKAGVYVVFQ-----LELRRVYBEGGGSVSL 163
Qy 188 ALRCLLEFSATAASSLGPQLCQVSG-----LIALRPESSLRRTLPWAHLK 235
Db 164 AIHLQPLRSAGAAGAAALTVLDPASSEARNASAFGQGRLLHLSAGRLGHHLHTEARAR 223
Qy 236 AAPFL-----TYFGLFQV 248
Db 224 HAWLTTQGATVQLGLFRV 240

RESULT 2

A75264

Hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 #text_change 03-Dec-1999 #text_change 17-Mar-2000

C:Accession: A75264

R.White, O.; Eisen, J.F.; Heidelberg, J.F.; Hickey, E.K.; Peterson, R.J.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Zalewski, C.; M.; Smith, H.O.; Venter, J.C.; Fraser, C.M.; Utterback, T.; Zalewski, C.; M.; Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

ALIGNMENTS

A; Reference number: A75250; MUID:20036896; PMID:10567266
 A; Accession: A75250
 A; Status: Preliminary
 A; Molecule type: DNA
 A; Residues: 1-375 <WHI>
 A; Cross-references: GB:AE002081; PIDN:AAF12062.1; PMID:9646034
 A; Experimental source: strain R1
 C; Genetics:
 A; Gene: DR216
 A; Map position: 1

Query Match 7.5%; Score 95; DB 2; Length 375;
 Best Local Similarity 23.9%; Pred. No. 2;
 Matches 64; Conservative 26; Mismatches 76; Indels 102; Gaps 12;

Qy 4 RRSQRRRGRRGEGFT--ALLVPLAIGLGLALAIGLGLASRSLSAQB-PAQEL 60
 Db 24 RRPGRAPORRGQGSHPARQLRADGAALA ---LVADVTRPLPAGELPPTLDL 77

~ 61 VAEEDQDPSEELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTARRAIAAHYEVHPR-PGQ 119
 Jb 78 AR ---QDLELDDDS---TDRLAQARAAATPRLPGD 108

Qy 120 DGAQAG--VDGTVSGWEARINNSPLRYNRQIGE----FIVTRAGLYLY-- 164
 Db 109 PGFPGFHPISGTLAIGLE-RISRAASDPAHAFQRGSVLGVADAAQEVYELVAGLFA 166

Qy 165 -----CQVHEDGKAVYLKDLLVGVIALRCLEEFSAATASSLGQLRCQVS-- 213
 Db 167 DWQPGEDRPPMPAHFQPGURLHL---PSATGEQTHLSLVAPG 204

Qy 214 -----GLLALRPGSSLRIRT 228
 Db 205 PGPRDPDMLPWQQLALTSGGSASRLFT 232

RESULT 3
 T16946 probable cation-transporting ATPase - Streptomyces coelicolor
 C; Species: Streptomyces coelicolor
 C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 18-Aug-2000
 C; Accession: T16946
 R; Seeger, K. J.; Harris, D.; Thomson, N.R.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, September 1999
 A; Reference number: 221607
 A; Status: Preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: DNA
 A; Experimental source: strain A3 (2)
 C; Genetics:
 A; Gene: SCOEDB:SC01.13
 C; Superfamily: ATPase nucleotide-binding domain homology <ATN>
 F; 442-585/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match 7.4%; Score 93.5; DB 2; Length 776;
 Best Local Similarity 24.1%; Pred. No. 6.1;
 Matches 63; Conservative 30; Mismatches 103; Indels 65; Gaps 11;

Qy 12 RRGEPGTALLVPLAIGLGLALA-CGLLLA-VVSLGSRASLSAQEPAQELVAAEDQDP 68
 Db 73 RRGAGVDLIAVLLGGTTLAVGETLAGVJIALMIGATGRTLEGAQRASHDILHALLAAP 132

Qy 69 SEUNPQTEESQDPAPFLNRLVRPRRSAPKGRKTARRAIAAHYEVHPRPGDGAQAGYVG 128
 Db 133 RSAARRRTGDD-----VVR----VPLSBEITGDAVVGPGEVNP-----VDG 169

Qy 129 TVSGWE--EARINSSPLRYNRQIGE----FIVTRAGLYLYCQVHDEGKAVYLKLDL 181
 Db 170 RVESTEAVLDEVSPLQVTRGEGARSQAVNAGGAFL-----RATAIEQDS 220

Qy 182 LVLGVIALRCLEEFSAATASSLGQLRCQ-----VSGLLALRPGSSLR--- 225

Db 221 TYAGTIVRL----ACQAGAESAPVVRLLADRYAAWFPLPLATATAALAMIVSGSAVAV 274
 A; Hypothetical protein C54D2.5 - Caenorhabditis elegans
 C; Species: Caenorhabditis elegans
 C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Mar-2000
 C; Accession: T15838
 R; Minx, P.
 submitted to the EMBL Data Library, October 1995
 A; Description: The sequence of C. elegans cosmid C54D2.
 A; Reference number: 218415
 A; Accession: T15838
 A; Status: Preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: DNA
 A; Residues: 1-1657 <MIN>
 A; Cross-references: EMBL:U37548; PID:91017804; PID:91017809; PID:AAA79201.1; CESP:CS54D
 C; Genetics:
 A; Introns: 40/2; 67/3; 86/3; 121/2; 199/3; 230/2; 308/2; 334/2; 370/2; 439/3; 470/3; 51
 C; Superfamily: sodium channel protein
 Query Match 7.4%; Score 93.5; DB 2; Length 1657;
 Best Local Similarity 23.2%; Pred. No. 15;
 Matches 63; Conservative 38; Mismatches 99; Indels 71; Gaps 12;
 Qy 17 GTAGLYPLAIGLGLAACLGL---ILLAVLVSGLGRAS----USAQEPAQEEVLAED 65
 Db 881 GNAQTINWAAALYFVALMTFGNIVFLNLLVAVLVEQFQESKEEKRQLEEDRKQAVEED 940
 Qy 66 QDPSELNPQTEESQDPAPFLNRLVRP-----RRSAPKGRKTRARRAIAAHYEVHPRPGQ 119
 Db 941 EKRELELIIKTTISPA---FNGVVAPECTCORPSSPE--BSPSPRLSAY- -HPSPER 994
 Qy 120 DGAQAGYDGTIVSGWEARINSSPL-----RYNRQIGEFVTRAGLYLYCQV 167
 Db 995 KHS-ANLDAAID-KRLVLRNSAPEDRSPVSEGRRDSRSLNRHASLIVLPVANGVpVpVQRV 1051
 Qy 168 H-----FDEKAVYLKLDLVDGVLALRCLE--EFSATAASSLGPQLRLCQV 212
 Db 1052 HSWKASQELKQQLAAEKKRNAAKQNTFVKLKKTCLHNRRPEFS----- 1095
 Qy 213 SGHLALRPGSSLRIRTLWPWHLKAAPFLTYF 243
 Db 1096 -LFLMGPKNPLRKCLQTTQKWFDTYTVL 1124

RESULT 5
 H87333 HlyD family secretion protein [imported] - Caulobacter crescentus
 C; Species: Caulobacter crescentus
 C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
 C; Accession: H87333
 R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.C.; B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Brumblaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.N.; Proc. Natl. Acad. Sci. U.S.A. 98, 4136-41, 2001
 A; Title: Complete Genome Sequence of Caulobacter crescentus.
 A; Reference number: A87249; MUID:21173698; PMID:11259647
 A; Accession: H87333
 A; Status: Preliminary
 A; Molecule type: DNA
 A; Residues: 1-378 <STO>
 A; Cross-references: GB:AE005673; PID:913421902; PMID:AAK22668.1; GSPDB:GN00148
 A; Genetics:
 A; Gene: CC0683